



US007358419B2

(12) **United States Patent**
Zinselmeier et al.

(10) **Patent No.:** **US 7,358,419 B2**
(45) **Date of Patent:** **Apr. 15, 2008**

(54) **ENHANCED SILK EXERTION UNDER STRESS**

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(*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 703 days.

(21) Appl. No.: **10/409,701**

(22) Filed: **Apr. 8, 2003**

(65) **Prior Publication Data**

US 2003/0221224 A1 Nov. 27, 2003

Related U.S. Application Data

(60) Provisional application No. 60/370,796, filed on Apr. 8, 2002.

(51) **Int. Cl.**

C12N 15/82 (2006.01)

C12N 15/70 (2006.01)

A01H 5/00 (2006.01)

(52) **U.S. Cl.** **800/287**; 435/320.1; 435/419; 536/24.1; 800/298

(58) **Field of Classification Search** None
See application file for complete search history.

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(57) **ABSTRACT**

The invention provides methods for enhancing maize silk exertion under stress conditions and compositions relating to such methods, including nucleic acids and proteins. The invention further provides recombinant expression cassettes, host cells, and transgenic plants.

13 Claims, No Drawings

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**ENHANCED SILK EXSERTION UNDER
STRESS**

REFERENCE TO RELATED APPLICATIONS

This application claims the benefit of, and hereby incorporates by reference, provisional patent application 60/370,796, filed Apr. 8, 2002.

TECHNICAL FIELD

The present invention relates generally to plant molecular biology. More specifically, it relates to nucleic acids and methods for modulating their expression in plants.

BACKGROUND OF THE INVENTION

Throughout their lives, plants are routinely subjected to a variety of stresses which act to impede or alter growth and development processes. Stress to the growth and development of agricultural plants has a negative economic impact in the form of reduced yields, increased expenditures to ameliorate the effects of stress, or both. Given the world's increasing human population and the diminishing land area available for agriculture, improving agricultural productivity is of paramount importance. Thus, there is a need for crop plants that are better able to tolerate stresses and maintain productivity under unfavorable conditions.

While traditional plant breeding approaches will continue to be important for improving agricultural plants, the new strategies that are likely to have the most significant impact on crop improvement will involve genetic engineering. A thorough understanding of the molecular and cellular mechanisms used by plants to avoid or tolerate stresses will aid in the development of new strategies to improve the stress tolerance of agricultural plants.

Stresses to plants may be caused by both biotic and abiotic agents. For example, biotic causes of stress include infection with a pathogen, insect feeding, parasitism by another plant such as mistletoe, and grazing by animals. Abiotic stresses include, for example, excessive or insufficient available water, insufficient light intensity, temperature extremes, synthetic chemicals such as herbicides, and excessive wind. Yet plants survive and often flourish, even under unfavorable conditions, using a variety of internal and external mechanisms for avoiding or tolerating stress. Plants' physiological responses to stress reflect changes in gene expression.

Grain yield in *Zea mays* is dependent upon the number of ovaries which are initiated, are fertilized, and develop to maturity. Reduced grain production may result from, inter alia, a decrease in the number of kernel initials, restricted or untimely silk exsertion, and/or kernel abortion during grain development.

Maize silks comprise the stigmatic tissues of the flower, intercepting air-borne pollen and supporting pollen tube growth to result in fertilization. Silk receptivity to pollen is limited in duration and is affected by environmental factors. For example, under drought conditions, silk exsertion is delayed or restricted and thus may not occur at the proper time relative to pollen shed. (See, for example, Herrero, M. P., and R. R. Johnson, *Crop Science* 21:105-110, 1981.) Importantly, the process of fertilization determines kernel number and thus sets an irreversible upper limit on grain yield.

What is needed in the art is a means to stabilize yield of maize across environments by ensuring ample and timely silk exsertion. This can be accomplished through transgenic

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modifications to create a plant with constant or increased rates of silk exsertion, even under stress, relative to an unmodified plant.

Modification of gene expression affecting silk growth and development requires use of promoters expressed exclusively or preferentially in silk tissues; for example, see U.S. Pat. No. 6,515,204. Also needed are coding regions capable of enhancing silk growth and development. The present invention meets these and other objectives.

SUMMARY OF THE INVENTION

Generally, it is an object of the present invention to provide methods of transforming plants with genetic constructs comprising novel combinations of appropriate promoter sequences and coding sequences to result in transformed plants with improved silk development under conditions of stress, relative to an untransformed plant under stress. Further objects of the present invention are to provide said transgenic plants exhibiting improved silk development under stress, and to provide said genetic constructs.

For example, cell division may be limiting to silk development under stress. Transformation with cytokinin biosynthetic genes would help to continue driving cell division in spite of stress to the plant. *Arabidopsis* plants transformed with *ipt* from *Agrobacterium tumefaciens* demonstrated increased flooding tolerance correlated with increased expression of *ipt*. (VanToai, T., et al., Abstract P518, Plant and Animal Genome VII Conference, San Diego, Calif., Jan. 17-21, 1999) Seed-specific expression of the *Agrobacterium tumefaciens* *tzs* gene in transgenic tobacco resulted in increased seed weight and number. (Roeckel, P., et al., *Physiologia Plantarum* 102:243-249, 1998) Dietrich et al., (*Plant Physiol. Biochem.* 33(3):327-336, 1995) showed that maximum cell division activity within developing maize endosperm coincided with the peak in total kernel cytokinin concentration. Thus, increasing cytokinin levels in the developing silk could serve to increase or maintain cell division and silk exsertion under stress conditions.

Alternatively or additionally, cell cycle genes, such as cyclin D, would help to continue driving cell division and thus maintain silk development in spite of stress to the plant. Cockcroft et al., (*Nature* 405:575-579, 2000) found that tobacco plants transformed with *CycD2* under control of a constitutive promoter had elevated overall growth rates. Riou-Khamlichi et al., (*Science* 283:1541-1544, 1999) reported that *CycD3* could induce cell division when constitutively expressed in transgenic *Arabidopsis* callus. Thus, increased expression of cell cycle genes specifically in silk tissue could promote cell division and silk growth.

Alternatively or additionally, transformation resulting in increased, directed expression of sucrose symporters could increase the carbon supply to developing silks. Symporters act to accumulate sucrose from the apoplast and transport it across cell boundaries, such as into phloem sieve elements or companion cells. Symporters may also transport monosaccharides, and their activity could be important in silk development, providing hexoses to elongating cells to maintain osmotic pressure and provide precursors for macromolecular synthesis. For a review, see Williams et al., *Trends in Plant Science* 5(7):283-290 (2000). There is evidence for tissue specificity and for transcriptional regulation of expression of sucrose symporters (Williams, supra, at pp. 287 and 289). Further, biotic and abiotic stresses can affect the expression of sucrose symporters. See, for example, Noiraud et al., *Plant Physiology* 122:1447-1455 (2000). Thus, constructs directing increased or sustained

expression of sucrose symporters in female reproductive tissues at critical developmental stages could be useful in maintaining growth and function of the silks. Leggewie et al., (U.S. Pat. No. 6,025,544) teach transformation with sucrose transporter sequences for earlier and/or more prolific flowering. The present invention, in contrast, provides transformation with sucrose transporter sequences to result in sustained or improved silk development under conditions of stress, especially drought, density and/or heat stress.

Alternatively or additionally, transformation resulting in targeted upregulation of invertases could increase the carbon supply to developing silks. Invertases convert sucrose into its component monosaccharides, glucose and fructose. Soluble invertase activity creating an increased solute concentration within a cell would serve to draw water into the cell and cause it to expand. In maize, a soluble invertase, *Ivr2*, has been shown to be specifically induced under water stress, and the resulting increase in hexose accumulation was speculated to increase osmotic pressure which could provide drought resistance. (Kim et al., *Plant Physiology* 124:71-84, 2000) Overexpression of *Ivr2* in silk tissues could therefore drive desirable cell expansion under conditions of water stress.

Alternatively or additionally, increased expression of a sodium antiporter within silk tissues could result in improved silk development under drought stress. Overexpression in *Brassica napus* of *AtNHX1*, encoding a vacuolar sodium antiporter from *Arabidopsis*, produces plants with reduced sensitivity to salt. Sodium ions are moved into the vacuole, increasing the solute concentration, which results in water being drawn into the cell. (Zhang et al., *PNAS* 98(22):12832-12836, 2001) Overexpression of *AtNHX1* or a gene encoding a protein of similar function within maize silk tissues could therefore drive increased water retention and desirable cell expansion under conditions of water stress. Such gene may be from maize.

Alternatively or additionally, adequate osmotic potential for cell expansion could result from directed overexpression of a vacuolar pyrophosphatase. Gaxiola et al., have reported that overexpression of the *Arabidopsis* *AVP1* gene, which encodes a vacuolar pyrophosphatase, resulted in marked drought tolerance, apparently through increased vacuolar accumulation of solute causing enhanced cellular water retention. (*PNAS* 98(20):11444-11449, 2001). Overexpression of *AVP1* or a gene encoding a protein of similar function within maize silk tissues could therefore drive increased water retention and desirable cell expansion under conditions of water stress.

Alternatively or additionally, expansins could help to drive silk cell expansion. Expansins are extracellular proteins which catalyze cell-wall enlargement by breaking non-covalent bonds between cell-wall polysaccharides. Increased expression of expansin genes has been correlated with rapid stem growth in submerged rice (Cho, H. T. & Kende, H., *Plant Cell* 9:1661-1671, 1997) and with root growth of maize seedlings under drought stress (Wu, Y. et al, *Plant Physiol.* 111:765-772, 1996). Directed expression of expansins could aid in cell enlargement, thus increasing silk length, particularly under stress conditions.

Alternatively or additionally, directed expression of aquaporins could aid in silk cell expansion. Aquaporins, designated TIPs (Tonoplast Intrinsic Proteins) or MIPs (plasma-Membrane Intrinsic Proteins), are channel proteins which facilitate water movement across vacuolar or plasma membranes. The maize aquaporin gene *ZmTIP1* is expressed at high levels in expanding cells, consistent with the hypothesis that TIPs allow rapid uptake of water. (Chaumont et al.,

Plant Physiol. 117:1143-1152, 1998) Upregulated and directed expression of aquaporins, including those endogenous to maize and particularly those expressed in maize silk tissue, could support rapid silk cell expansion and thus promote silk tissue growth. See also U.S. Pat. Nos. 6,313,375 and 6,313,376, hereby incorporated by reference.

Alternatively or additionally, targeted expression of genes encoding enzymes involved in raffinose synthase may provide tolerance of drought, salinity, and/or cold. Taji et al., (*Plant Journal* 29(4):417-426, 2002) have reported that "stress-inducible galactinol synthase plays a key role in the accumulation of galactinol and raffinose under abiotic stress conditions" and that "galactinol and raffinose may function as osmoprotectants in drought-stress tolerance of plants." Therefore, constructs directing overexpression of galactinol synthase or raffinose synthase in silk tissue could lead to improved silk exertion under abiotic stress.

It is a further object of the invention to provide promoter sequences active exclusively or preferentially in silks and methods of use of the promoter sequences. In other aspects the present invention relates to: 1) recombinant expression cassettes, comprising a nucleic acid of the present invention operably linked to a promoter, 2) a host cell into which has been introduced the recombinant expression cassette, and 3) a transgenic plant comprising the recombinant expression cassette. The host cell and plant are optionally from maize.

It is a further object of the present invention to provide a method of improved control of expression of an endogenous or exogenous product in a transformed plant or its progeny.

It is a further object of the present invention to provide a method for effecting useful changes in the phenotype of a transformed plant or its progeny.

It is a further object of the present invention to provide a method for modulating the development of a transformed plant or its progeny.

In a further aspect, the present invention relates to a method for modulating gene expression in a stably transformed plant comprising the steps of (a) transforming a plant cell with a recombinant expression cassette of the present invention; (b) growing the plant cell under appropriate growing conditions and (c) regenerating a stably transformed plant from the plant cell wherein said linked nucleotide sequence is expressed.

DETAILED DESCRIPTION OF THE INVENTION

Overview

A. Nucleic Acids and Proteins of the Present Invention

Unless otherwise stated, the polynucleotide and polypeptide sequences identified in SEQ ID NOS: 1-26 represent exemplary polynucleotides and polypeptides useful in the present invention. Table 1 provides identification of SEQ ID NOS: 1-26.

Gene Name	Polynucleotide SEQ ID NO.	Polypeptide SEQ ID NO.
Silk-preferred promoter ("gl2")	1, 26	—
Isopentenyl transferase	2	3
Cyclin D	4	5
Cyclin-dependent kinase	6	7
α -expansin	8	9
β -expansin	10	11
Aquaporin	12	13

-continued

Gene Name	Polynucleotide SEQ ID NO.	Polypeptide SEQ ID NO.
Aquaporin	14	15
Aquaporin	16	17
Sucrose symporter	18	19
Soluble invertase	20	21
Sodium antiporter	22	23
Vacuolar pyrophosphatase	24	25

B. Exemplary Utility of the Present Invention

The present invention provides utility in such exemplary applications as engineering *Zea mays* plants to exhibit improved silk exertion, relative to a non-transformed plant, under conditions of environmental stress, such as drought, high plant density, or excessive heat.

Improved silk exertion may comprise elements of time-liness and quality, for example, more rapid exertion, greater silk length, and more complete and/or more uniform silk emergence from the ear shoot. Such improvements in silk exertion may result from, for example, increased rates of cell division in silk tissue, increased expansion of cells composing silks, and altered rates of flow of water and solutes within or into silk tissue.

Definitions

Units, prefixes, and symbols may be denoted in their SI accepted form. Unless otherwise indicated, nucleic acids are written left to right in 5' to 3' orientation; amino acid sequences are written left to right in amino to carboxy orientation, respectively. Numeric ranges recited within the specification are inclusive of the numbers defining the range and include each integer within the defined range. Amino acids may be referred to herein by either their commonly known three-letter symbols or by the one-letter symbols recommended by the IUPAC-IUBMB Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes. Unless otherwise provided for, software, electrical, and electronics terms as used herein are as defined in The New IEEE Standard Dictionary of Electrical and Electronics Terms (5th edition, 1993). The terms defined below are more fully defined by reference to the specification as a whole. Section headings provided throughout the specification are not limitations to the various objects and embodiments of the present invention.

By "amplified" is meant the construction of multiple copies of a nucleic acid sequence or multiple copies complementary to the nucleic acid sequence using at least one of the nucleic acid sequences as a template. Amplification systems include the polymerase chain reaction (PCR) system, ligase chain reaction (LCR) system, nucleic acid sequence based amplification (NASBA, Cangene, Mississauga, Ontario), Q-Beta Replicase systems, transcription-based amplification system (TAS), and strand displacement amplification (SDA). See, e.g., *Diagnostic Molecular Microbiology: Principles and Applications*, D. H. Persing et al., Ed., American Society for Microbiology, Washington, D.C. (1993). The product of amplification is termed an amplicon.

As used herein, "antisense orientation" includes reference to a duplex polynucleotide sequence that is operably linked to a promoter in an orientation where the antisense strand is transcribed. The antisense strand is sufficiently complementary to an endogenous transcription product such that translation of the endogenous transcription product is often inhibited.

By "encoding" or "encoded", with respect to a specified nucleic acid, is meant comprising the information for translation into the specified protein. A nucleic acid encoding a protein may comprise intervening sequences (e.g., introns) within translated regions of the nucleic acid, or may lack such intervening sequences (e.g., as in cDNA). The information by which a protein is encoded is specified by the use of codons. Typically, the amino acid sequence is encoded by the nucleic acid using the "universal" genetic code. However, variants of the universal code, such as are present in some plant, animal, and fungal mitochondria, the bacterium *Mycoplasma capricolum*, or the ciliate Macronucleus, may be used when the nucleic acid is expressed therein.

When the nucleic acid is prepared or altered synthetically, advantage can be taken of known codon preferences of the intended host organism. For example, although nucleic acid sequences of the present invention may be expressed in both monocotyledonous and dicotyledonous plant species, sequences can be modified to account for the specific codon preferences and GC content preferences of monocotyledons or dicotyledons as these preferences have been shown to differ (Murray et al., *Nucl. Acids Res.* 17: 477-498 (1989)). Thus, the maize-preferred codon for a particular amino acid may be derived from known gene sequences from maize. Maize codon usage for 28 genes from maize plants is listed in Table 4 of Murray et al., supra.

As used herein "full-length sequence" in reference to a specified polynucleotide or its encoded protein means having the entire amino acid sequence of a native (non-synthetic), endogenous, biologically (e.g., structurally or catalytically) active form of the specified protein. Methods to determine whether a sequence is full-length are well known in the art, including such exemplary techniques as northern or western blots, primer extension, S1 protection, and ribonuclease protection. See, e.g., *Plant Molecular Biology: A Laboratory Manual*, Clark, Ed., Springer-Verlag, Berlin (1997). Comparison to known full-length homologous (orthologous and/or paralogous) sequences can also be used to identify full-length sequences of the present invention. Additionally, consensus sequences typically present at the 5' and 3' untranslated regions of mRNA aid in the identification of a polynucleotide as full-length. For example, the consensus sequence ANNNNAUGG, where the underlined codon represents the N-terminal methionine, aids in determining whether the polynucleotide has a complete 5' end. Consensus sequences at the 3' end, such as polyadenylation sequences, aid in determining whether the polynucleotide has a complete 3' end.

As used herein, "heterologous" in reference to a nucleic acid is a nucleic acid that originates from a foreign species, or, if from the same species, is substantially modified from its native form in composition and/or genomic locus by human intervention. For example, a promoter operably linked to a heterologous structural gene is from a species different from that from which the structural gene was derived, or, if from the same species, one or both are substantially modified from their original form. A heterologous protein may originate from a foreign species or, if from the same species, is substantially modified from its original form by human intervention.

By "host cell" is meant a cell which contains a vector and supports the replication and/or expression of the vector. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells. Preferably, host cells are monocotyledonous or dicotyledonous plant cells. A particularly preferred monocotyledonous host cell is a maize host cell.

The term “introduced” includes reference to the incorporation of a nucleic acid into a eukaryotic or prokaryotic cell where the nucleic acid may be incorporated into the genome of the cell (e.g., chromosome, plasmid, plastid or mitochondrial DNA), converted into an autonomous replicon, or transiently expressed (e.g., transfected mRNA). The term includes such nucleic acid introduction means as “transfection”, “transformation” and “transduction”.

The term “isolated” refers to material, such as a nucleic acid or a protein, which is substantially free from components that normally accompany or interact with it in its naturally-occurring environment. The isolated material optionally comprises material not found with the material in its natural environment, or if the material is in its natural environment, the material has been synthetically (non-naturally) altered by human intervention to a composition and/or placed at a location in the cell (e.g., genome or subcellular organelle) not native to the isolated material. The alteration to yield the synthetic material can be performed on the material within or removed from its natural state. For example, a naturally-occurring nucleic acid becomes an isolated nucleic acid if it is altered, or if it is transcribed from DNA which has been altered, by means of human intervention performed within the cell from which it originates. See, e.g., Compounds and Methods for Site Directed Mutagenesis in Eukaryotic Cells, Kmiec, U.S. Pat. No. 5,565,350; In Vivo Homologous Sequence Targeting in Eukaryotic Cells; Zarling et al., PCT/US93/03868. Likewise, a naturally-occurring nucleic acid (e.g., a promoter) becomes isolated if it is introduced by non-naturally-occurring means to a locus of the genome not native to that nucleic acid.

As used herein, “nucleic acid” includes reference to a deoxyribonucleotide or ribonucleotide polymer, or chimeras thereof, in either single- or double-stranded form, and unless otherwise limited, encompasses known analogues having the essential nature of natural nucleotides in that they hybridize to single-stranded nucleic acids in a manner similar to that of naturally-occurring nucleotides (e.g., peptide nucleic acids).

By “nucleic acid library” is meant a collection of isolated DNA or RNA molecules which comprise and substantially represent the entire transcribed fraction of a genome of a specified organism, or of a tissue or cell type from that organism. Construction of exemplary nucleic acid libraries, such as genomic and cDNA libraries, is taught in standard molecular biology references such as Berger and Kimmel, *Guide to Molecular Cloning Techniques, Methods in Enzymology*, Vol. 152, Academic Press, Inc., San Diego, Calif. (Berger); Sambrook et al., *Molecular Cloning—A Laboratory Manual*, 2nd ed., Vol. 1-3 (1989); and *Current Protocols in Molecular Biology*, F. M. Ausubel et al., Eds., Current Protocols, a joint venture between Greene Publishing Associates, Inc. and John Wiley & Sons, Inc. (1994).

As used herein “operably linked” includes reference to a functional linkage between a promoter and a second sequence, wherein the promoter sequence initiates and mediates transcription of the second sequence. Generally, operably linked means that the nucleic acid sequences being linked are contiguous and, where necessary to join two protein coding regions, contiguous and in the same reading frame.

As used herein, the term “plant” includes reference to whole plants, plant organs (e.g., leaves, stems, roots, etc.), seeds and plant cells and progeny of same. Plant cell, as used herein includes, without limitation, cells isolated from seeds, suspension cultures, embryos, meristematic regions, callus tissue, leaves, roots, shoots, gametophytes, sporophytes,

pollen, and microspores. The class of plants which can be used in the methods of the invention include both monocotyledonous and dicotyledonous plants. A particularly preferred plant is *Zea mays*.

As used herein, “polynucleotide” includes reference to a deoxyribopolynucleotide, ribopolynucleotide, or chimeras or analogs thereof that have the essential nature of a natural deoxy- or ribo-nucleotide in that they hybridize, under stringent hybridization conditions, to substantially the same nucleotide sequence as do naturally-occurring nucleotides and/or allow translation into the same amino acid(s) as do the naturally-occurring nucleotide(s). A polynucleotide can be full-length or a subsequence of a native or heterologous structural or regulatory gene. Unless otherwise indicated, the term includes reference to the specified sequence as well as to the complementary sequence thereof. Thus, DNAs or RNAs with backbones modified for stability or for other reasons are “polynucleotides” as that term is intended herein. Moreover, DNAs or RNAs comprising unusual bases, such as inosine, or modified bases, such as tritylated bases, to name just two examples, are polynucleotides as the term is used herein. It will be appreciated that a great variety of modifications have been made to DNA and RNA that serve many useful purposes known to those of skill in the art. The term polynucleotide as it is employed herein embraces such chemically, enzymatically or metabolically modified forms of polynucleotides, as well as the chemical forms of DNA and RNA characteristic of viruses and cells, including among other things, simple and complex cells.

The terms “polypeptide”, “peptide” and “protein” are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to naturally-occurring amino acid polymers, as well as to amino acid polymers in which one or more amino acid residue is an artificial chemical analogue of a corresponding naturally-occurring amino acid. The essential nature of such analogues of naturally-occurring amino acids is that, when incorporated into a protein, that protein is specifically reactive to antibodies elicited to the same protein but consisting entirely of naturally-occurring amino acids. The terms “polypeptide”, “peptide” and “protein” are also inclusive of modifications including, but not limited to, glycosylation, lipid attachment, sulfation, gamma-carboxylation of glutamic acid residues, hydroxylation and ADP-ribosylation. Further, this invention contemplates the use of both the methionine-containing and the methionine-less amino terminal variants of proteins of the invention.

As used herein “promoter” includes reference to a region of DNA upstream from the start of transcription and involved in recognition and binding of RNA polymerase and other proteins to initiate transcription. A “plant promoter” is a promoter capable of initiating transcription in plant cells whether or not its origin is a plant cell. Exemplary plant promoters include, but are not limited to, those that are obtained from plants, plant viruses, and bacteria which comprise genes expressed in plant cells such *Agrobacterium* or *Rhizobium*. Examples of promoters under developmental control include promoters that preferentially initiate transcription in certain tissues, such as leaves, roots, or seeds. Such promoters are referred to as “tissue preferred”. Promoters which initiate transcription only in certain tissue are referred to as “tissue specific”. A “cell type” specific promoter primarily drives expression in certain cell types in one or more organs, for example, vascular cells in roots or leaves. An “inducible” or “repressible” promoter is a promoter which is under environmental control. Examples of environmental conditions that may effect transcription by

inducible promoters include anaerobic conditions or the presence of light. Tissue specific, tissue preferred, cell type specific, and inducible promoters constitute the class of “non-constitutive” promoters. A “constitutive” promoter is a promoter which is active under most conditions.

As used herein “recombinant” includes reference to a cell or vector that has been modified by the introduction of a heterologous nucleic acid or to a cell derived from a cell so modified. Thus, for example, recombinant cells express genes that are not found in identical form within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under-expressed or not expressed at all, as a result of human intervention. The term “recombinant” as used herein does not encompass the alteration of the cell or vector by naturally-occurring events (e.g., spontaneous mutation, natural transformation/transduction/transposition) such as those occurring without human intervention.

As used herein, a “recombinant expression cassette” is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements which permit transcription of a particular nucleic acid in a host cell. The recombinant expression cassette can be incorporated into a plasmid, chromosome, mitochondrial DNA, plastid DNA, virus, or nucleic acid fragment. Typically, the recombinant expression cassette portion of an expression vector includes, among other sequences, a promoter and a nucleic acid to be transcribed.

The terms “residue” and “amino acid residue” and “amino acid” are used interchangeably herein to refer to an amino acid that is incorporated into a protein, polypeptide, or peptide (collectively “protein”). The amino acid may be a naturally-occurring amino acid and, unless otherwise limited, may encompass non-natural analogs of natural amino acids that can function in a similar manner as naturally-occurring amino acids.

The term “selectively hybridizes” includes reference to hybridization, under stringent hybridization conditions, of a nucleic acid sequence to a specified nucleic acid target sequence to a detectably greater degree (e.g., at least 2-fold over background) than its hybridization to non-target nucleic acid sequences and to the substantial exclusion of non-target nucleic acids. Selectively hybridizing sequences typically have about at least 80% sequence identity, preferably 90% sequence identity, and most preferably 100% sequence identity (i.e., are complementary) with each other.

The term “stringent conditions” or “stringent hybridization conditions” includes reference to conditions under which a probe will selectively hybridize to its target sequence to a detectably greater degree than to other sequences (e.g., at least 2-fold over background). Stringent conditions are sequence-dependent and will be different in different circumstances. By controlling the stringency of the hybridization and/or washing conditions, target sequences can be identified which are 100% complementary to the probe (homologous probing). Alternatively, stringency conditions can be adjusted to allow some mismatching in sequences so that lower degrees of similarity are detected (heterologous probing). Generally, a probe is less than about 1000 nucleotides in length, optionally less than 500 nucleotides in length.

Typically, stringent conditions will be those in which the salt concentration is less than about 1.5 M Na ion, typically about 0.01 to 1.0 M Na ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C. for short probes (e.g., 10 to 50 nucleotides) and at least about 60° C. for long probes (e.g., greater than 50 nucleotides).

Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. Exemplary low stringency conditions include hybridization with a buffer solution of 30 to 35% formamide, 1 M NaCl, 1% SDS (sodium dodecyl sulphate) at 37° C., and a wash in 1× to 2×SSC (20×SSC=3.0 M NaCl/0.3 M trisodium citrate) at 50 to 55° C. Exemplary moderate stringency conditions include hybridization in 40 to 45% formamide, 1 M NaCl, 1% SDS at 37° C., and a wash in 0.5× to 1×SSC at 55 to 60° C. Exemplary high stringency conditions include hybridization in 50% formamide, 1 M NaCl, 1% SDS at 37° C., and a wash in 0.1×SSC at 60 to 65° C.

Specificity is typically the function of post-hybridization washes, the critical factors being the ionic strength and temperature of the final wash solution. For DNA-DNA hybrids, the T_m can be approximated from the equation of Meinkoth and Wahl, *Anal. Biochem.*, 138:267-284 (1984): $T_m = 81.5^\circ \text{C.} + 16.6 (\log M) + 0.41 (\% \text{ GC}) - 0.61 (\% \text{ form}) - 500/L$; where M is the molarity of monovalent cations, % GC is the percentage of guanosine and cytosine nucleotides in the DNA, % form is the percentage of formamide in the hybridization solution, and L is the length of the hybrid in base pairs. The T_m is the temperature (under defined ionic strength and pH) at which 50% of a complementary target sequence hybridizes to a perfectly matched probe. T_m is reduced by about 1° C. for each 1% of mismatching; thus, T_m , hybridization and/or wash conditions can be adjusted to hybridize to sequences of the desired identity. For example, if sequences with $\geq 90\%$ identity are sought, the T_m can be decreased 10° C. Generally, stringent conditions are selected to be about 5° C. lower than the thermal melting point (T_m) for the specific sequence and its complement at a defined ionic strength and pH. However, severely stringent conditions can utilize a hybridization and/or wash at 1, 2, 3, or 4° C. lower than the thermal melting point (T_m); moderately stringent conditions can utilize a hybridization and/or wash at 6, 7, 8, 9, or 10° C. lower than the thermal melting point (T_m); low stringency conditions can utilize a hybridization and/or wash at 11, 12, 13, 14, 15, or 20° C. lower than the thermal melting point (T_m). Using the equation, hybridization and wash compositions, and desired T_m , those of ordinary skill will understand that variations in the stringency of hybridization and/or wash solutions are inherently described. If the desired degree of mismatching results in a T_m of less than 45° C. (aqueous solution) or 32° C. (formamide solution) it is preferred to increase the SSC concentration so that a higher temperature can be used. Hybridization and/or wash conditions can be applied for at least 10, 30, 60, 90, 120, or 240 minutes. An extensive guide to the hybridization of nucleic acids is found in Tijssen, *Laboratory Techniques in Biochemistry and Molecular Biology—Hybridization with Nucleic Acid Probes*, Part I, Chapter 2 “Overview of principles of hybridization and the strategy of nucleic acid probe assays”, Elsevier, New York (1993); and *Current Protocols in Molecular Biology*, Chapter 2, Ausubel, et al., Eds., Greene Publishing and Wiley-Interscience, New York (1995).

As used herein, “transgenic plant” includes reference to a plant which comprises within its genome a heterologous polynucleotide. Generally, the heterologous polynucleotide is stably integrated within the genome such that the polynucleotide is passed on to successive generations. The heterologous polynucleotide may be integrated into the genome alone or as part of a recombinant expression cassette. “Transgenic” is used herein to include any cell, cell line, callus, tissue, plant part or plant, the genotype of which has been altered by the presence of heterologous nucleic

acid including those transgenics initially so altered as well as those created by sexual crosses or asexual propagation from the initial transgenic. The term "transgenic" as used herein does not encompass the alteration of the genome (chromosomal or extra-chromosomal) by conventional plant breeding methods or by naturally-occurring events such as random cross-fertilization, non-recombinant viral infection, non-recombinant bacterial transformation, non-recombinant transposition, or spontaneous mutation.

As used herein, "vector" includes reference to a nucleic acid used in introduction of a polynucleotide of the present invention into a host cell. Vectors are often replicons. Expression vectors permit transcription of a nucleic acid inserted therein.

The following terms are used to describe the sequence relationships between a polynucleotide/polypeptide of the present invention with a reference polynucleotide/polypeptide: (a) "reference sequence", (b) "comparison window", (c) "sequence identity", and (d) "percentage of sequence identity".

(a) As used herein, "reference sequence" is a defined sequence used as a basis for sequence comparison with a polynucleotide/polypeptide of the present invention. A reference sequence may be a subset or the entirety of a specified sequence; for example, as a segment of a full-length cDNA or gene sequence, or the complete cDNA or gene sequence.

(b) As used herein, "comparison window" includes reference to a contiguous and specified segment of a polynucleotide/polypeptide sequence, wherein the polynucleotide/polypeptide sequence may be compared to a reference sequence and wherein the portion of the polynucleotide/polypeptide sequence in the comparison window may comprise additions or deletions (i.e., gaps) compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. Generally, the comparison window is at least 20 contiguous nucleotides/amino acids residues in length, and optionally can be 30, 40, 50, 100, 200, 300, 400, 500, 600, 750, 1000, 1250, 1500, or longer. Those of skill in the art understand that to avoid a high similarity to a reference sequence due to inclusion of gaps in the polynucleotide/polypeptide sequence, a gap penalty is typically introduced and is subtracted from the number of matches.

Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison may be conducted by the local homology algorithm of Smith and Waterman, *Adv. Appl. Math.* 2: 482 (1981); by the homology alignment algorithm of Needleman and Wunsch, *J. Mol. Biol.* 48: 443 (1970); by the search for similarity method of Pearson and Lipman, *Proc. Natl. Acad. Sci.* 85: 2444 (1988); by computerized implementations of these programs, including, but not limited to: CLUSTAL in the PC/Gene program by Intelligenetics, Mountain View, Calif.; GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, Wis., USA. The CLUSTAL program is well described by Higgins and Sharp, *Gene* 73: 237-244 (1988); Higgins and Sharp, *CABIOS* 5: 151-153 (1989); Corpet, et al., *Nucleic Acids Research* 16: 10881-90 (1988); Huang, et al., *Computer Applications in the Biosciences* 8: 155-65 (1992), and Pearson, et al., *Methods in Molecular Biology* 24: 307-331 (1994).

The BLAST family of programs which can be used for database similarity searches includes: BLASTN for nucleotide query sequences against nucleotide database sequences; BLASTX for nucleotide query sequences against

protein database sequences; BLASTP for protein query sequences against protein database sequences; TBLASTN for protein query sequences against nucleotide database sequences; and TBLASTX for nucleotide query sequences against nucleotide database sequences. See, *Current Protocols in Molecular Biology*, Chapter 19, Ausubel, et al., Eds., Greene Publishing and Wiley-Interscience, New York (1995); Altschul et al., *J. Mol. Biol.*, 215:403-410 (1990); and, Altschul et al., *Nucleic Acids Res.* 25:3389-3402 (1997).

Software for performing BLAST analyses is publicly available, e.g., through the National Center for Biotechnology Information. This program involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold. These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0) and N (penalty score for mismatching residues; always <0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST program parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100, M=5, N=4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff (1989) *Proc. Natl. Acad. Sci. USA* 89:10915).

In addition to calculating percent sequence identity, the BLAST program also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin & Altschul, *Proc. Nat'l. Acad. Sci. USA* 90:5873-5877 (1993)). One measure of similarity provided by the BLAST program is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance.

BLAST searches assume that proteins can be modeled as random sequences. However, many real proteins comprise regions of nonrandom sequences which may be homopolymeric tracts, short-period repeats, or regions enriched in one or more amino acids. Such low-complexity regions may be aligned between unrelated proteins even though other regions of the protein are entirely dissimilar. A number of low-complexity filter programs can be employed to reduce such low-complexity alignments. For example, the SEG (Wooten and Federhen, *Comput. Chem.*, 17:149-163 (1993)) and XNU (Claverie and States, *Comput. Chem.*, 17:191-201 (1993)) low-complexity filters can be employed alone or in combination.

Unless otherwise stated, nucleotide and protein identity/similarity values provided herein are calculated using GAP (GCG Version 10) under default values.

GAP (Global Alignment Program) can also be used to compare a polynucleotide or polypeptide of the present invention with a reference sequence. GAP uses the algorithm of Needleman and Wunsch (*J. Mol. Biol.* 48: 443-453, 1970) to find the alignment of two complete sequences that maximizes the number of matches and minimizes the number of gaps. GAP considers all possible alignments and gap positions and creates the alignment with the largest number of matched bases and the fewest gaps. It allows for the provision of a gap creation penalty and a gap extension penalty in units of matched bases. GAP must make a profit of gap creation penalty number of matches for each gap it inserts. If a gap extension penalty greater than zero is chosen, GAP must, in addition, make a profit for each gap inserted of the length of the gap times the gap extension penalty. Default gap creation penalty values and gap extension penalty values in Version 10 of the Wisconsin Genetics Software Package for protein sequences are 8 and 2, respectively. For nucleotide sequences the default gap creation penalty is 50 while the default gap extension penalty is 3. For polypeptide sequences the default gap creation penalty is 8 while the default gap extension penalty is 2. The gap creation and gap extension penalties can be expressed as an integer selected from the group of integers consisting of from 0 to 100. Thus, for example, the gap creation and gap extension penalties can each independently be: 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 30, 40, 50, 60 or greater.

GAP presents one member of the family of best alignments. There may be many members of this family, but no other member has a better quality. GAP displays four figures of merit for alignments: Quality, Ratio, Identity, and Similarity. The Quality is the metric maximized in order to align the sequences. Ratio is the quality divided by the number of bases in the shorter segment. Percent Identity is the percent of the symbols that actually match. Percent Similarity is the percent of the symbols that are similar. Symbols that are across from gaps are ignored. A similarity is scored when the scoring matrix value for a pair of symbols is greater than or equal to 0.50, the similarity threshold. The scoring matrix used in Version 10 of the Wisconsin Genetics Software Package is BLOSUM62 (see Henikoff & Henikoff (1989) *Proc. Natl. Acad. Sci. USA* 89:10915).

Multiple alignment of the sequences can be performed using the CLUSTAL method of alignment (Higgins and Sharp (1989) *CABIOS*. 5:151-153) with the default parameters (GAP PENALTY=10, GAP LENGTH PENALTY=10). Default parameters for pairwise alignments using the CLUSTAL method are KTUPLE 1, GAP PENALTY=3, WINDOW=5 and DIAGONALS SAVED=5.

(c) As used herein, "sequence identity" or "identity" in the context of two nucleic acid or polypeptide sequences includes reference to the residues in the two sequences which are the same when aligned for maximum correspondence over a specified comparison window. When percentage of sequence identity is used in reference to proteins it is recognized that residue positions which are not identical often differ by conservative amino acid substitutions, where amino acid residues are substituted for other amino acid residues with similar chemical properties (e.g. charge or hydrophobicity) and therefore do not change the functional properties of the molecule. Where sequences differ in conservative substitutions, the percent sequence identity may be adjusted upwards to correct for the conservative nature of the substitution. Sequences which differ by such conservative substitutions are said to have "sequence similarity" or "similarity". Means for making this adjustment are well-known to those of skill in the art. Typically this involves

scoring a conservative substitution as a partial rather than a full mismatch, thereby increasing the percentage sequence identity. Thus, for example, where an identical amino acid is given a score of 1 and a non-conservative substitution is given a score of zero, a conservative substitution is given a score between zero and 1. The scoring of conservative substitutions is calculated, e.g., according to the algorithm of Meyers and Miller, *Computer Applic. Biol. Sci.*, 4: 11-17 (1988) e.g., as implemented in the program PC/GENE (Intelligenetics, Mountain View, Calif., USA).

(d) As used herein, "percentage of sequence identity" means the value determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity.

Utilities

The present invention provides, among other things, compositions and methods for modulating (i.e., increasing or decreasing) the level of polynucleotides and polypeptides of the present invention in plants. In particular, the polynucleotides and polypeptides of the present invention can be expressed temporally or spatially, e.g., at developmental stages, in tissues, and/or in quantities, which are uncharacteristic of non-recombinantly engineered plants.

The present invention also provides isolated nucleic acids comprising polynucleotides of sufficient length and complementarity to a polynucleotide of the present invention to use as probes or amplification primers in the detection, quantitation, or isolation of gene transcripts. For example, isolated nucleic acids of the present invention can be used as probes in detecting deficiencies in the level of mRNA in screenings for desired transgenic plants, for detecting mutations in the gene (e.g., substitutions, deletions, or additions), for monitoring upregulation of expression or changes in enzyme activity in screening assays of compounds, for detection of any number of allelic variants (polymorphisms), orthologs, or paralogs of the gene, or for site directed mutagenesis in eukaryotic cells (see, e.g., U.S. Pat. No. 5,565,350). The isolated nucleic acids of the present invention can also be used for recombinant expression of their encoded polypeptides, or for use as immunogens in the preparation and/or screening of antibodies. The isolated nucleic acids of the present invention can also be employed for use in sense or antisense suppression of one or more genes of the present invention in a host cell, tissue, or plant. Attachment of chemical agents which bind, intercalate, cleave and/or crosslink to the isolated nucleic acids of the present invention can also be used to modulate transcription or translation.

The present invention also provides isolated proteins comprising a polypeptide of the present invention (e.g., preproenzyme, proenzyme, or enzymes). The present invention also provides proteins comprising at least one epitope from a polypeptide of the present invention. The proteins of the present invention can be employed in assays for enzyme agonists or antagonists of enzyme function, or for use as immunogens or antigens to obtain antibodies specifically immunoreactive with a protein of the present invention.

Such antibodies can be used in assays for expression levels, for identifying and/or isolating nucleic acids of the present invention from expression libraries, for identification of homologous polypeptides from other species, or for purification of polypeptides of the present invention.

The isolated nucleic acids and polypeptides of the present invention can be used over a broad range of plant types, particularly monocots such as the species of the family Gramineae including *Hordeum*, *Secale*, *Oryza*, *Triticum*, *Sorghum* (e.g., *S. bicolor*) and *Zea* (e.g., *Z. mays*), and dicots such as Glycine.

The isolated nucleic acid and proteins of the present invention can also be used in species from the genera: *Cucurbita*, *Rosa*, *Vitis*, *Juglans*, *Fragaria*, *Lotus*, *Medicago*, *Onobrychis*, *Trifolium*, *Trigonella*, *Vigna*, *Citrus*, *Linum*, *Geranium*, *Manihot*, *Daucus*, *Arabidopsis*, *Brassica*, *Raphanus*, *Sinapis*, *Atropa*, *Capsicum*, *Datura*, *Hyoscyamus*, *Lycopersicon*, *Nicotiana*, *Solanum*, *Petunia*, *Digitalis*, *Majorana*, *Ciahorium*, *Helianthus*, *Lactuca*, *Bromus*, *Asparagus*, *Antirrhinum*, *Heterocallis*, *Nemesis*, *Pelargonium*, *Panicum*, *Pennisetum*, *Ranunculus*, *Senecio*, *Salpiglossis*, *Cucumis*, *Browallia*, *Pisum*, *Phaseolus*, *Lolium*, and *Avena*.

Nucleic Acids

The present invention provides, among other things, isolated nucleic acids of RNA, DNA, and analogs and/or chimeras thereof, comprising a polynucleotide of the present invention.

A polynucleotide of the present invention is inclusive of those in Table 1 and:

(a) an isolated polynucleotide encoding a polypeptide of the present invention such as those referenced in Table 1, including exemplary polynucleotides of the present invention;

(b) an isolated polynucleotide which is the product of amplification from a plant nucleic acid library using primer pairs which selectively hybridize under stringent conditions to loci within a polynucleotide of the present invention;

(c) an isolated polynucleotide which selectively hybridizes to a polynucleotide of (a) or (b);

(d) an isolated polynucleotide having a specified sequence identity with polynucleotides of (a), (b), or (c);

(e) an isolated polynucleotide encoding a protein having a specified number of contiguous amino acids from a prototype polypeptide, wherein the protein is specifically recognized by antisera elicited by presentation of the protein and wherein the protein does not detectably immunoreact to antisera which has been fully immunosorbed with the protein;

(f) complementary sequences of polynucleotides of (a), (b), (c), (d), or (e);

(g) an isolated polynucleotide comprising at least a specific number of contiguous nucleotides from a polynucleotide of (a), (b), (c), (d), (e), or (f);

(h) an isolated polynucleotide from a full-length enriched cDNA library having the physico-chemical property of selectively hybridizing to a polynucleotide of (a), (b), (c), (d), (e), (f), or (g); and

(i) an isolated polynucleotide made by the process of: 1) providing a full-length enriched nucleic acid library, 2) selectively hybridizing the polynucleotide to a polynucleotide of (a), (b), (c), (d), (e), (f), (g), or (h), thereby isolating the polynucleotide from the nucleic acid library.

A. Polynucleotides Encoding A Polypeptide of the Present Invention

As indicated in (a), above, the present invention provides isolated nucleic acids comprising a polynucleotide of the present invention, wherein the polynucleotide encodes a polypeptide of the present invention. Every nucleic acid sequence herein that encodes a polypeptide also, by reference to the genetic code, describes every possible silent variation of the nucleic acid. One of ordinary skill will recognize that each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine; and UGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally identical molecule. Thus, each silent variation of a nucleic acid which encodes a polypeptide of the present invention is implicit in each described polypeptide sequence and is within the scope of the present invention. Accordingly, the present invention includes polynucleotides of the present invention and polynucleotides encoding a polypeptide of the present invention.

B. Polynucleotides Amplified from a Plant Nucleic Acid Library

As indicated in (b), above, the present invention provides an isolated nucleic acid comprising a polynucleotide of the present invention, wherein the polynucleotides are amplified, under nucleic acid amplification conditions, from a plant nucleic acid library. Nucleic acid amplification conditions for each of the variety of amplification methods are well known to those of ordinary skill in the art. The plant nucleic acid library can be constructed from a monocot such as a cereal crop. Exemplary cereals include corn, sorghum, wheat, or rice. The plant nucleic acid library can also be constructed from a dicot such as soybean, alfalfa, or canola. *Zea mays* lines B73, PHRE1, A632, BMS-P2#10, W23, and Mo17 are known and publicly available. Other publicly known and available maize lines can be obtained from the Maize Genetics Cooperation (Urbana, Ill.). Wheat lines are available from the Wheat Genetics Resource Center (Manhattan, Kan.).

The nucleic acid library may be a cDNA library, a genomic library, or a library generally constructed from nuclear transcripts at any stage of intron processing. In optional embodiments, the cDNA library is constructed using an enriched full-length cDNA synthesis method. Examples of such methods include Oligo-Capping (Maruyama, K. and Sugano, S. *Gene* 138: 171-174, 1994), Biotinylated CAP Trapper (Carninci, et al., *Genomics* 37: 327-336, 1996), and CAP Retention Procedure (Edery, E., Chu, L. L., et al., *Molecular and Cellular Biology* 15: 3363-3371, 1995). Rapidly growing tissues or rapidly dividing cells are preferred for use as an mRNA source for construction of a cDNA library. Growth stages of corn are described in "How a Corn Plant Develops," Special Report No. 48, Iowa State University of Science and Technology Cooperative Extension Service, Ames, Iowa, Reprinted February 1993.

A polynucleotide of this embodiment (or subsequences thereof) can be obtained, for example, by using amplification primers which are selectively hybridized and primer extended, under nucleic acid amplification conditions, to at least two sites within a polynucleotide of the present invention, or to two sites within the nucleic acid which flank and comprise a polynucleotide of the present invention, or to a site within a polynucleotide of the present invention and a site within the nucleic acid which comprises it. Methods for obtaining 5' and/or 3' ends of a vector insert are well known in the art. See, e.g., RACE (Rapid Amplification of Comple-

mentary Ends) as described in Frohman, M. A., in PCR Protocols: A Guide to Methods and Applications, M. A. Innis, D. H. Gelfand, J. J. Sninsky, T. J. White, Eds. (Academic Press, Inc., San Diego), pp. 28-38 (1990)); see also, U.S. Pat. No. 5,470,722, and *Current Protocols in Molecular Biology*, Unit 15.6, Ausubel, et al., Eds., Greene Publishing and Wiley-Interscience, New York (1995); Frohman and Martin, *Techniques* 1:165 (1989).

Optionally, the primers are complementary to a subsequence of the target nucleic acid which they amplify but may have a sequence identity ranging from about 85% to 99% relative to the polynucleotide sequence to which they are designed to anneal. As those skilled in the art will appreciate, the sites to which the primer pairs will selectively hybridize are chosen such that a single contiguous nucleic acid can be formed under the desired nucleic acid amplification conditions. The primer length as measured in contiguous nucleotides is selected from the group of integers consisting of from at least 15 to 50. Thus, the primers can be at least 15, 18, 20, 25, 30, 40, or 50 contiguous nucleotides in length. Those of skill will recognize that a lengthened primer sequence can be employed to increase specificity of binding (i.e., annealing) to a target sequence. A non-annealing sequence at the 5' end of a primer (a "tail") can be added, for example, to introduce a cloning site at the terminal ends of the amplicon.

The amplification products can be translated using expression systems well known to those of skill in the art. The resulting translation products can be confirmed as polypeptides of the present invention by, for example, assaying for the appropriate catalytic activity (e.g., specific activity and/or substrate specificity), or verifying the presence of one or more epitopes which are specific to a polypeptide of the present invention. Methods for protein synthesis from PCR-derived templates are known in the art and available commercially. See, e.g., Amersham Life Sciences, Inc, Catalog '97, p. 354.

C. Polynucleotides Which Selectively Hybridize to a Polynucleotide of (A) or (B)

As indicated in (c), above, the present invention provides isolated nucleic acids comprising polynucleotides of the present invention, wherein the polynucleotides selectively hybridize, under selective hybridization conditions, to a polynucleotide of sections (A) or (B) as discussed above. Thus, the polynucleotides of this embodiment can be used for isolating, detecting, and/or quantifying nucleic acids comprising the polynucleotides of (A) or (B). For example, polynucleotides of the present invention can be used to identify, isolate, or amplify partial or full-length clones in a deposited library. In some embodiments, the polynucleotides are genomic or cDNA sequences isolated or otherwise complementary to a cDNA from a dicot or monocot nucleic acid library. Exemplary species of monocots and dicots include, but are not limited to: maize, canola, soybean, cotton, wheat, sorghum, sunflower, alfalfa, oats, sugar cane, millet, barley, and rice. The cDNA library comprises at least 50% to 95% full-length sequences (for example, at least 50%, 60%, 70%, 80%, 90%, or 95% full-length sequences). The cDNA libraries can be normalized to increase the representation of rare sequences. See, e.g., U.S. Pat. No. 5,482,845. Low stringency hybridization conditions are typically, but not exclusively, employed with sequences having a reduced sequence identity relative to complementary sequences. Moderate and high stringency conditions can optionally be employed for sequences of greater identity.

Low stringency conditions allow selective hybridization of sequences having about 70% to 80% sequence identity and can be employed to identify orthologous or paralogous sequences.

D. Polynucleotides Having a Specific Sequence Identity with the Polynucleotides of (A), (B) or (C)

As indicated in (d), above, the present invention provides isolated nucleic acids comprising polynucleotides of the present invention, wherein the polynucleotides have a specified identity at the nucleotide level to a polynucleotide as disclosed above in sections (A), (B), or (C), above. Identity can be calculated using, for example, the BLAST, CLUSTALW, or GAP programs under default conditions. The percentage of identity to a reference sequence is at least 60% and, rounded upwards to the nearest integer, can be expressed as an integer selected from the group of integers consisting of from 60 to 99. Thus, for example, the percentage of identity to a reference sequence can be at least 70%, 75%, 80%, 85%, 90%, or 95%.

The polynucleotides/polypeptides of the present invention having a specified sequence identity with a polynucleotide/polypeptide of section (A), (B), or (C) can be of a length (measured in contiguous nucleotides or amino acids) selected from the group consisting of from 15 to the length of the polynucleotide/polypeptide of (A), (B), or (C) or any integer value in between. For example, the length of the polynucleotides or polypeptides can be 25, 50, 75, 100, 150, 200, 250, 300, 350, 400, 500, 750, 1000, 1250, 1500, or greater.

Optionally, the polynucleotides of this embodiment will encode a polypeptide that will share an epitope with a polypeptide encoded by the polynucleotides of sections (A), (B), or (C). Thus, these polynucleotides encode a first polypeptide which elicits production of antisera comprising antibodies which are specifically reactive to a second polypeptide encoded by a polynucleotide of (A), (B), or (C). However, the first polypeptide does not bind to antisera raised against itself when the antisera has been fully immunosorbed with the first polypeptide. Hence, the polynucleotides of this embodiment can be used to generate antibodies for use in, for example, the screening of expression libraries for nucleic acids comprising polynucleotides of (A), (B), or (C), or for purification of, or in immunoassays for, polypeptides encoded by the polynucleotides of (A), (B), or (C). The polynucleotides of this embodiment comprise nucleic acid sequences which can be employed for selective hybridization to a polynucleotide encoding a polypeptide of the present invention.

Screening polypeptides for specific binding to antisera can be conveniently achieved using peptide display libraries. This method involves the screening of large collections of peptides for individual members having the desired function or structure. Antibody screening of peptide display libraries is well known in the art. The displayed peptide sequences can be from 3 to 5000 or more amino acids in length, frequently from 5-100 amino acids long, and often from about 8 to 15 amino acids long. In addition to direct chemical synthetic methods for generating peptide libraries, several recombinant DNA methods have been described. One type involves the display of a peptide sequence on the surface of a bacteriophage or cell. Each bacteriophage or cell contains the nucleotide sequence encoding the particular displayed peptide sequence. Such methods are described in PCT patent publication Nos. 91/17271, 91/18980, 91/19818, and 93/08278. Other systems for generating libraries of peptides have aspects of both in vitro chemical synthesis and

recombinant methods. See, PCT Patent publication Nos. 92/05258, 92/14843, and 97/20078. See also, U.S. Pat. Nos. 5,658,754; and 5,643,768. Peptide display libraries, vectors, and screening kits are commercially available from such suppliers as Invitrogen (Carlsbad, Calif.).

E. Polynucleotides Encoding a Protein Having a Subsequence from a Prototype Polypeptide and Cross-Reactive to the Prototype Polypeptide

As indicated in (e), above, the present invention provides isolated nucleic acids comprising polynucleotides of the present invention, wherein the polynucleotides encode a protein having a subsequence of contiguous amino acids from a prototype polypeptide of the present invention such as are provided in (a), above. The length of contiguous amino acids from the prototype polypeptide is selected from the group of integers consisting of from at least 10 to the number of amino acids within the prototype sequence. Thus, for example, the polynucleotide can encode a polypeptide having a subsequence having at least 10, 15, 20, 25, 30, 35, 40, 45, or 50, contiguous amino acids from the prototype polypeptide. Further, the number of such subsequences encoded by a polynucleotide of the instant embodiment can be any integer selected from the group consisting of from 0 to 20, such as 2, 3, 4, or 5. The subsequences can be separated by any integer of nucleotides from 0 to the number of nucleotides in the sequence such as at least 5, 10, 15, 25, 50, 100, or 200 nucleotides.

The proteins encoded by polynucleotides of this embodiment, when presented as an immunogen, elicit the production of polyclonal antibodies which specifically bind to a prototype polypeptide such as but not limited to, a polypeptide encoded by the polynucleotide of (a) or (b), above. Generally, however, a protein encoded by a polynucleotide of this embodiment does not bind to antisera raised against the prototype polypeptide when the antisera has been fully immunosorbed with the prototype polypeptide. Methods of making and assaying for antibody binding specificity/affinity are well known in the art. Exemplary immunoassay formats include ELISA, competitive immunoassays, radioimmunoassays, Western blots, indirect immunofluorescent assays and the like.

In a preferred assay method, fully immunosorbed and pooled antisera which is elicited to the prototype polypeptide can be used in a competitive binding assay to test the protein. The concentration of the prototype polypeptide required to inhibit 50% of the binding of the antisera to the prototype polypeptide is determined. If the amount of the protein required to inhibit binding is less than twice the amount of the prototype protein, then the protein is said to specifically bind to the antisera elicited to the immunogen. Accordingly, the proteins of the present invention embrace allelic variants, conservatively modified variants, and minor recombinant modifications to a prototype polypeptide.

A polynucleotide of the present invention optionally encodes a protein having a molecular weight as the non-glycosylated protein within 20% of the molecular weight of the full-length non-glycosylated polypeptides of the present invention. Molecular weight can be readily determined by SDS-PAGE under reducing conditions. Optionally, the molecular weight is within 15% of a full length polypeptide of the present invention, more preferably within 10% or 5%, and most preferably within 3%, 2%, or 1% of a full length polypeptide of the present invention.

Optionally, the polynucleotides of this embodiment will encode a protein having a specific enzymatic activity at least 50%, 60%, 80%, or 90% of a cellular extract comprising the

native, endogenous full-length polypeptide of the present invention. Further, the proteins encoded by polynucleotides of this embodiment will optionally have a substantially similar affinity constant (K_m) and/or catalytic activity (i.e., the microscopic rate constant, k_{cat}) as the native endogenous, full-length protein. Those of skill in the art will recognize that k_{cat}/K_m value determines the specificity for competing substrates and is often referred to as the specificity constant. Proteins of this embodiment can have a k_{cat}/K_m value at least 10% of a full-length polypeptide of the present invention as determined using the endogenous substrate of that polypeptide. Optionally, the k_{cat}/K_m value will be at least 20%, 30%, 40%, 50%, and most preferably at least 60%, 70%, 80%, 90%, or 95% the k_{cat}/K_m value of the full-length polypeptide of the present invention. Determination of k_{cat} , K_m , and k_{cat}/K_m can be determined by any number of means well known to those of skill in the art. For example, the initial rates (i.e., the first 5% or less of the reaction) can be determined using rapid mixing and sampling techniques (e.g., continuous-flow, stopped-flow, or rapid quenching techniques), flash photolysis, or relaxation methods (e.g., temperature jumps) in conjunction with such exemplary methods of measuring as spectrophotometry, spectrofluorimetry, nuclear magnetic resonance, or radioactive procedures. Kinetic values are conveniently obtained using a Lineweaver-Burk or Eadie-Hofstee plot.

F. Polynucleotides Complementary to the Polynucleotides of (A)-(E)

As indicated in (f), above, the present invention provides isolated nucleic acids comprising polynucleotides complementary to the polynucleotides of paragraphs A-E, above. As those of skill in the art will recognize, complementary sequences base-pair throughout the entirety of their length with the polynucleotides of sections (A)-(E) (i.e., have 100% sequence identity over their entire length). Complementary bases associate through hydrogen bonding in double stranded nucleic acids. For example, the following base pairs are complementary: guanine and cytosine; adenine and thymine; and adenine and uracil.

G. Polynucleotides Which are Subsequences of the Polynucleotides of (A)-(F)

As indicated in (g), above, the present invention provides isolated nucleic acids comprising polynucleotides which comprise at least 15 contiguous bases from the polynucleotides of sections (A) through (F) as discussed above. The length of the polynucleotide is given as an integer selected from the group consisting of from at least 15 to the length of the nucleic acid sequence of which the polynucleotide is a subsequence. Thus, for example, polynucleotides of the present invention are inclusive of polynucleotides comprising at least 15, 20, 25, 30, 40, 50, 60, 75, 100, 200, 300, 400, 500, 600, 700, 800, 900, or 1000 contiguous nucleotides in length from the polynucleotides of (A)-(F). Optionally, the number of such subsequences encoded by a polynucleotide of the instant embodiment can be any integer selected from the group consisting of from 1 to 20, such as 2, 3, 4, or 5. The subsequences can be separated by any integer of nucleotides from 1 to the number of nucleotides in the sequence such as at least 5, 10, 15, 25, 50, 100, or 200 nucleotides.

Subsequences can be made by in vitro synthetic, in vitro biosynthetic, or in vivo recombinant methods. In optional embodiments, subsequences can be made by nucleic acid amplification. For example, nucleic acid primers will be constructed to selectively hybridize to a sequence (or its complement) within, or co-extensive with, the coding region.

A subsequence of the present invention can comprise structural characteristics of the sequence from which it is derived. Alternatively, a subsequence can lack certain structural characteristics of the larger sequence from which it is derived such as a poly (A) tail. Optionally, a subsequence from a polynucleotide encoding a polypeptide having at least one epitope in common with a prototype polypeptide sequence as provided in (a), above, may encode an epitope in common with the prototype sequence. Alternatively, the subsequence may not encode an epitope in common with the prototype sequence but can be used to isolate the larger sequence by, for example, nucleic acid hybridization with the sequence from which it is derived. Subsequences can be used to modulate or detect gene expression by introducing into the subsequences compounds which bind, intercalate, cleave and/or crosslink to nucleic acids. Exemplary compounds include acridine, psoralen, phenanthroline, naphthoquinone, daunomycin or chloroethylaminoaryl conjugates.

H. Polynucleotides From a Full-length Enriched cDNA Library Having the Physico-Chemical Property of Selectively Hybridizing to a Polynucleotide of (A)-(G)

As indicated in (h), above, the present invention provides an isolated polynucleotide from a full-length enriched cDNA library having the physico-chemical property of selectively hybridizing to a polynucleotide of paragraphs (A), (B), (C), (D), (E), (F), or (G) as discussed above. Methods of constructing full-length enriched cDNA libraries are known in the art and discussed briefly below. The cDNA library comprises at least 50% to 95% full-length sequences (for example, at least 50%, 60%, 70%, 80%, 90%, or 95% full-length sequences). The cDNA library can be constructed from a variety of tissues from a monocot or dicot at a variety of developmental stages. Exemplary species include maize, wheat, rice, canola, soybean, cotton, sorghum, sunflower, alfalfa, oats, sugar cane, millet, barley, and rice. Methods of selectively hybridizing a polynucleotide from a full-length enriched library to a polynucleotide of the present invention are known to those of ordinary skill in the art. Any number of stringency conditions can be employed to allow for selective hybridization. In optional embodiments, the stringency allows for selective hybridization of sequences having at least 70%, 75%, 80%, 85%, 90%, 95%, or 98% sequence identity over the length of the hybridized region.

I. Polynucleotide Products Made by a cDNA Isolation Process

As indicated in (I), above, the present invention provides an isolated polynucleotide made by the process of: 1) providing a full-length enriched nucleic acid library, 2) selectively hybridizing the polynucleotide to a polynucleotide of paragraphs (A), (B), (C), (D), (E), (F), (G), or (H) as discussed above, and thereby isolating the polynucleotide from the nucleic acid library. Full-length enriched nucleic acid libraries are constructed as discussed in paragraph (G) and below. Selective hybridization conditions are as discussed in paragraph (G). Nucleic acid purification procedures are well known in the art. Purification can be conveniently accomplished using solid-phase methods; such methods are well known to those of skill in the art and kits are available from commercial suppliers such as Advanced Biotechnologies (Surrey, UK). For example, a polynucleotide of paragraphs (A)-(H) can be immobilized to a solid support such as a membrane, bead, or particle. See, e.g., U.S. Pat. No. 5,667,976. The polynucleotide product of the present process is selectively hybridized to an immobilized polynucleotide and the solid support is subsequently isolated from non-hybridized polynucleotides by methods including,

but not limited to, centrifugation, magnetic separation, filtration, electrophoresis, and the like.

Construction of Nucleic Acids

The isolated nucleic acids of the present invention can be made using (a) standard recombinant methods, (b) synthetic techniques, or combinations thereof. In some embodiments, the polynucleotides of the present invention will be cloned, amplified, or otherwise constructed from a monocot such as corn, rice, or wheat, or a dicot such as soybean.

The nucleic acids may conveniently comprise sequences in addition to a polynucleotide of the present invention. For example, a multi-cloning site comprising one or more endonuclease restriction sites may be inserted into the nucleic acid to aid in isolation of the polynucleotide. Also, translatable sequences may be inserted to aid in the isolation of the translated polynucleotide of the present invention. For example, a hexa-histidine marker sequence provides a convenient means to purify the proteins of the present invention. A polynucleotide of the present invention can be attached to a vector, adapter, or linker for cloning and/or expression of a polynucleotide of the present invention. Additional sequences may be added to such cloning and/or expression sequences to optimize their function in cloning and/or expression, to aid in isolation of the polynucleotide, or to improve the introduction of the polynucleotide into a cell. Typically, the length of a nucleic acid of the present invention is less than 20 kilobase pairs, often less than 15 kb, and frequently less than 10 kb. Use of cloning vectors, expression vectors, adapters, and linkers is well known and extensively described in the art. For a description of various nucleic acids see, for example, Stratagene Cloning Systems, Catalogs 1999 (La Jolla, Calif.); and, Amersham Life Sciences, Inc, Catalog '99 (Arlington Heights, Ill.).

A. Recombinant Methods for Constructing Nucleic Acids

The isolated nucleic acid compositions of this invention, such as RNA, cDNA, genomic DNA, or a hybrid thereof, can be obtained from plant biological sources using any number of cloning methodologies known to those of skill in the art. In some embodiments, oligonucleotide probes which selectively hybridize, under stringent conditions, to the polynucleotides of the present invention are used to identify the desired sequence in a cDNA or genomic DNA library. Isolation of RNA and construction of cDNA and genomic libraries are well known to those of ordinary skill in the art. See, e.g., *Plant Molecular Biology: A Laboratory Manual*, Clark, Ed., Springer-Verlag, Berlin (1997); and, *Current Protocols in Molecular Biology*, Ausubel, et al., Eds., Greene Publishing and Wiley-Interscience, New York (1995).

A1. Full-length Enriched cDNA Libraries

A number of cDNA synthesis protocols have been described which provide enriched full-length cDNA libraries. Enriched full-length cDNA libraries are constructed to comprise at least 60%, and more preferably at least 70%, 80%, 90% or 95% full-length inserts amongst clones containing inserts. The length of insert in such libraries can be at least 2, 3, 4, 5, 6, 7, 8, 9, 10 or more kilobase pairs. Vectors to accommodate inserts of these sizes are known in the art and available commercially. See, e.g., Stratagene's lambda ZAP Express (cDNA cloning vector with 0 to 12 kb cloning capacity). An exemplary method of constructing a greater than 95% pure full-length cDNA library is described by Carninci et al., *Genomics*, 37:327-336 (1996). Other methods for producing full-length libraries are known in the art.

See, e.g., Edery et al., *Mol. Cell Biol.*, 15(6):3363-3371 (1995); and, PCT Application WO 96/34981.

A2 Normalized or Subtracted cDNA Libraries

A non-normalized cDNA library represents the mRNA population of the tissue from which it was made. Since unique clones are out-numbered by clones derived from highly expressed genes, their isolation can be laborious. Normalization of a cDNA library is the process of creating a library in which each clone is more equally represented. Construction of normalized libraries is described in Ko, *Nucl. Acids Res.*, 18(19):5705-5711 (1990); Patanjali et al., *Proc. Natl. Acad. U.S.A.*, 88:1943-1947 (1991); U.S. Pat. Nos. 5,482,685, 5,482,845, and 5,637,685. In an exemplary method described by Soares et al., normalization resulted in reduction of the abundance of clones from a range of four orders of magnitude to a narrow range of only 1 order of magnitude. *Proc. Natl. Acad. Sci. USA*, 91:9228-9232 (1994).

Subtracted cDNA libraries are another means to increase the proportion of less abundant cDNA species. In this procedure, cDNA prepared from one pool of mRNA is depleted of sequences present in a second pool of mRNA by hybridization. The cDNA:mRNA hybrids are removed and the remaining un-hybridized cDNA pool is enriched for sequences unique to that pool. See, Foote et al., in, *Plant Molecular Biology: A Laboratory Manual*, Clark, Ed., Springer-Verlag, Berlin (1997); Kho and Zarbl, *Technique*, 3(2):58-63 (1991); Sive and St. John, *Nucl. Acids Res.*, 16(22):10937 (1988); *Current Protocols in Molecular Biology*, Ausubel, et al., Eds., Greene Publishing and Wiley-Interscience, New York (1995); and, Swaroop et al., *Nucl. Acids Res.*, 19(8):1954 (1991). cDNA subtraction kits are commercially available. See, e.g., PCR-Select (Clontech, Palo Alto, Calif.).

To construct genomic libraries, large segments of genomic DNA are generated by fragmentation, e.g. using restriction endonucleases, and are ligated with vector DNA to form concatemers that can be packaged into the appropriate vector. Methodologies to accomplish these ends, and sequencing methods to verify the sequence of nucleic acids, are well known in the art. Examples of appropriate molecular biological techniques and instructions sufficient to direct persons of skill through many construction, cloning, and screening methodologies are found in Sambrook, et al., *Molecular Cloning: A Laboratory Manual*, 2nd Ed., Cold Spring Harbor Laboratory Vols. 1-3 (1989), *Methods in Enzymology*, Vol. 152: *Guide to Molecular Cloning Techniques*, Berger and Kimmel, Eds., San Diego: Academic Press, Inc. (1987), *Current Protocols in Molecular Biology*, Ausubel, et al., Eds., Greene Publishing and Wiley-Interscience, New York (1995); *Plant Molecular Biology: A Laboratory Manual*, Clark, Ed., Springer-Verlag, Berlin (1997). Kits for construction of genomic libraries are also commercially available.

The cDNA or genomic library can be screened using a probe based upon the sequence of a polynucleotide of the present invention such as those disclosed herein. Probes may be used to hybridize with genomic DNA or cDNA sequences to isolate homologous genes in the same or different plant species. Those of skill in the art will appreciate that various degrees of stringency of hybridization can be employed in the assay, and either the hybridization or the wash medium can be stringent.

The nucleic acids of interest can also be amplified from nucleic acid samples using amplification techniques. For instance, polymerase chain reaction (PCR) technology can

be used to amplify the sequences of polynucleotides of the present invention and related genes directly from genomic DNA or cDNA libraries. PCR and other in vitro amplification methods may also be useful, for example, to clone nucleic acid sequences that code for proteins to be expressed, to make nucleic acids to use as probes for detecting the presence of the desired mRNA in samples, for nucleic acid sequencing, or for other purposes. The T4 gene 32 protein (Boehringer Mannheim) can be used to improve yield of long PCR products.

PCR-based screening methods have been described. Wilfinger et al., describe a PCR-based method in which the longest cDNA is identified in the first step so that incomplete clones can be eliminated from study. *BioTechniques*, 22(3): 481-486 (1997). Such methods are particularly effective in combination with a full-length cDNA construction methodology, above.

B. Synthetic Methods for Constructing Nucleic Acids

The isolated nucleic acids of the present invention can also be prepared by direct chemical synthesis by methods such as the phosphotriester method of Narang et al., *Meth. Enzymol.* 68: 90-99 (1979); the phosphodiester method of Brown et al., *Meth. Enzymol.* 68: 109-151 (1979); the diethylphosphoramidite method of Beaucage et al., *Tetra. Lett.* 22: 1859-1862 (1981); the solid phase phosphoramidite triester method described by Beaucage and Caruthers, *Tetra. Letts.* 22(20): 1859-1862 (1981), e.g., using an automated synthesizer, e.g., as described in Needham-VanDevanter et al., *Nucleic Acids Res.*, 12: 6159-6168 (1984); and, the solid support method of U.S. Pat. No. 4,458,066. Chemical synthesis generally produces a single-stranded oligonucleotide. This may be converted into double-stranded DNA by hybridization with a complementary sequence, or by polymerization with a DNA polymerase using the single strand as a template. One of skill will recognize that while chemical synthesis of DNA is best employed for sequences of about 100 bases or less, longer sequences may be obtained by the ligation of shorter sequences.

Recombinant Expression Cassettes

The present invention further provides recombinant expression cassettes comprising a nucleic acid of the present invention. A nucleic acid sequence coding for the desired polypeptide of the present invention, for example a cDNA or a genomic sequence encoding a full-length polypeptide of the present invention, can be used to construct a recombinant expression cassette which can be introduced into the desired host cell. A recombinant expression cassette will typically comprise a polynucleotide of the present invention operably linked to transcriptional initiation regulatory sequences which will direct the transcription of the polynucleotide in the intended host cell, such as within tissues of a transformed plant.

For example, plant expression vectors may include (1) a cloned plant gene under the transcriptional control of 5' and 3' regulatory sequences and (2) a dominant selectable marker. Such plant expression vectors may also contain, if desired, a promoter regulatory region (e.g., one conferring inducible or constitutive, environmentally- or developmentally-regulated, or cell- or tissue-specific/selective expression), a transcription initiation start site, a ribosome binding site, an RNA processing signal, a transcription termination site, and/or a polyadenylation signal.

A plant promoter fragment can be employed which will direct expression of a polynucleotide of the present invention in all tissues of a regenerated plant. Such promoters are referred to herein as "constitutive" promoters and are active

under most environmental conditions and states of development or cell differentiation. Examples of constitutive promoters include the cauliflower mosaic virus (CaMV) 35S transcription initiation region, the 1'- or 2'-promoter derived from T-DNA of *Agrobacterium tumefaciens*, the ubiquitin 1 promoter, the Smas promoter, the cinnamyl alcohol dehydrogenase promoter (U.S. Pat. No. 5,683,439), the Nos promoter, the pEmu promoter, the rubisco promoter, and the GRP1-8 promoter.

Alternatively, the plant promoter can direct expression of a polynucleotide of the present invention in a specific tissue or may be otherwise under more precise environmental or developmental control. Such promoters are referred to here as "inducible" promoters. Environmental conditions that may effect transcription by inducible promoters include pathogen attack, anaerobic conditions, or the presence of light. Examples of inducible promoters are the Adh1 promoter which is inducible by hypoxia or cold stress, the Hsp70 promoter which is inducible by heat stress, and the PPKK promoter which is inducible by light.

Examples of promoters under developmental control include promoters that initiate transcription only, or preferentially, in certain tissues, such as leaves, roots, fruit, seeds, or flowers. Exemplary promoters include the anther specific promoter 5126 (U.S. Pat. Nos. 5,689,049 and 5,689,051), glob-1 promoter, and gamma-zein promoter. The present invention provides promoters with expression limited to, or enhanced in, maize silks, including the gl2 promoter (SEQ ID NO: 1 and SEQ ID NO: 26). The operation of a promoter may also vary depending on its location in the genome. Thus, an inducible promoter may become fully or partially constitutive in certain locations.

Both heterologous and non-heterologous (i.e., endogenous) promoters can be employed to direct expression of the nucleic acids of the present invention. These promoters can also be used, for example, in recombinant expression cassettes to drive expression of antisense nucleic acids to reduce, increase, or alter concentration and/or composition of the proteins of the present invention in a desired tissue. Thus, in some embodiments, the nucleic acid construct will comprise a promoter, functional in a plant cell, operably linked to a polynucleotide of the present invention. Promoters useful in these embodiments include the endogenous promoters driving expression of a polypeptide of the present invention.

In some embodiments, isolated nucleic acids which serve as promoter or enhancer elements can be introduced in the appropriate position (generally upstream) of a non-heterologous form of a polynucleotide of the present invention so as to up- or down-regulate expression of a polynucleotide of the present invention. For example, endogenous promoters can be altered in vivo by mutation, deletion, and/or substitution (see, Kmiec, U.S. Pat. No. 5,565,350; Zarling et al., PCT/US93/03868), or isolated promoters can be introduced into a plant cell in the proper orientation and distance from a cognate gene of a polynucleotide of the present invention so as to control the expression of the gene. Gene expression can be modulated under conditions suitable for plant growth so as to alter the total concentration and/or alter the composition of the polypeptides of the present invention in plant cell. Thus, the present invention provides compositions, and methods for making, heterologous promoters and/or enhancers operably linked to a native, endogenous (i.e., non-heterologous) form of a polynucleotide of the present invention.

If polypeptide expression is desired, it is generally desirable to include a polyadenylation region at the 3'-end of a

polynucleotide coding region. The polyadenylation region can be derived from the natural gene, from a variety of other plant genes, or from T-DNA. The 3' end sequence to be added can be derived from, for example, the nopaline synthase or octopine synthase genes, or alternatively from another plant gene, or less preferably from any other eukaryotic gene.

An intron sequence can be added to the 5' untranslated region or the coding sequence to increase the amount of the mature message that accumulates in the cytosol. Inclusion of a spliceable intron in the transcription unit in both plant and animal expression constructs has been shown to increase gene expression at both the mRNA and protein levels up to 1000-fold. Buchman and Berg, *Mol. Cell Biol.* 8: 4395-4405 (1988); Callis et al., *Genes Dev.* 1: 1183-1200 (1987). Such intron enhancement of gene expression is typically greatest when placed near the 5' end of the transcription unit. Use of maize introns Adh1-S intron 1, 2, and 6, the Bronze-1 intron are known in the art. See generally, *The Maize Handbook*, Chapter 116, Freeling and Walbot, Eds., Springer, New York (1994). The vector comprising the sequences from a polynucleotide of the present invention will typically comprise a marker gene which confers a selectable phenotype on plant cells. Typical vectors useful for expression of genes in higher plants are well known in the art and include vectors derived from the tumor-inducing (Ti) plasmid of *Agrobacterium tumefaciens* described by Rogers et al., *Meth. in Enzymol.*, 153:253-277 (1987).

A polynucleotide of the present invention can be expressed in either sense or anti-sense orientation as desired. It will be appreciated that control of gene expression in either sense or anti-sense orientation can have a direct impact on the observable plant characteristics. Antisense technology can be conveniently used to inhibit gene expression in plants. To accomplish this, a nucleic acid segment from the desired gene is cloned and operably linked to a promoter such that the anti-sense strand of RNA will be transcribed. The construct is then transformed into plants and the antisense strand of RNA is produced. In plant cells, it has been shown that antisense RNA inhibits gene expression by preventing the accumulation of mRNA which encodes the enzyme of interest, see, e.g., Sheehy et al., *Proc. Nat'l. Acad. Sci. (USA)* 85: 8805-8809 (1988); and Hiatt et al., U.S. Pat. No. 4,801,340.

Another method of suppression is sense suppression (i.e., co-suppression). Introduction of nucleic acid configured in the sense orientation has been shown to be an effective means by which to block the transcription of target genes. For an example of the use of this method to modulate expression of endogenous genes, see Napoli et al., *The Plant Cell* 2: 279-289 (1990) and U.S. Pat. No. 5,034,323.

Catalytic RNA molecules or ribozymes can also be used to inhibit expression of plant genes. It is possible to design ribozymes that specifically pair with virtually any target RNA and cleave the phosphodiester backbone at a specific location, thereby functionally inactivating the target RNA. In carrying out this cleavage, the ribozyme is not itself altered, and is thus capable of recycling and cleaving other molecules, making it a true enzyme. The inclusion of ribozyme sequences within antisense RNAs confers RNA-cleaving activity upon them, thereby increasing the activity of the constructs. The design and use of target RNA-specific ribozymes is described in Haseloff et al., *Nature* 334: 585-591 (1988).

A variety of cross-linking agents, alkylating agents and radical generating species as pendant groups on polynucleotides of the present invention can be used to bind, label,

detect, and/or cleave nucleic acids. For example, Vlassov, V. V., et al., *Nucleic Acids Res* (1986) 14:4065-4076, describe covalent bonding of a single-stranded DNA fragment with alkylating derivatives of nucleotides complementary to target sequences. A report of similar work by the same group is that by Knorre, D. G., et al., *Biochimie* (1985) 67:785-789. Iverson and Dervan also showed sequence-specific cleavage of single-stranded DNA mediated by incorporation of a modified nucleotide which was capable of activating cleavage (*J. Am Chem Soc* (1987) 109:1241-1243). Meyer, R. B., et al., *J. Am Chem Soc* (1989) 111:8517-8519, effect covalent crosslinking to a target nucleotide using an alkylating agent complementary to the single-stranded target nucleotide sequence. A photoactivated crosslinking to single-stranded oligonucleotides mediated by psoralen was disclosed by Lee, B. L., et al., *Biochemistry* (1988) 27:3197-3203. Use of crosslinking in triple-helix forming probes was also disclosed by Home, et al., *J. Am Chem Soc* (1990) 112:2435-2437. Use of N4, N4-ethanocytosine as an alkylating agent to crosslink to single-stranded oligonucleotides has also been described by Webb and Matteucci, *J. Am Chem Soc* (1986) 108:2764-2765; *Nucleic Acids Res* (1986) 14:7661-7674; Feteritz et al., *J. Am. Chem. Soc.* 113:4000 (1991). Various compounds to bind, detect, label, and/or cleave nucleic acids are known in the art. See, for example, U.S. Pat. Nos. 5,543,507; 5,672,593; 5,484,908; 5,256,648; and, 5,681,941.

Proteins

The isolated proteins of the present invention comprise a polypeptide having at least 10 amino acids from a polypeptide of the present invention (or conservative variants thereof) such as those encoded by any one of the polynucleotides of the present invention as discussed more fully above (e.g., Table 1). The proteins of the present invention or variants thereof can comprise any number of contiguous amino acid residues from a polypeptide of the present invention, wherein that number is selected from the group of integers consisting of from 10 to the number of residues in a full-length polypeptide of the present invention. Optionally, this subsequence of contiguous amino acids is at least 15, 20, 25, 30, 35, or 40 amino acids in length, often at least 50, 60, 70, 80, or 90 amino acids in length. Further, the number of such subsequences can be any integer selected from the group consisting of from 1 to 20, such as 2, 3, 4, or 5.

The present invention further provides a protein comprising a polypeptide having a specified sequence identity/similarity with a polypeptide of the present invention. The percentage of sequence identity/similarity is an integer selected from the group consisting of from 50 to 99. Exemplary sequence identity/similarity values include 60%, 65%, 70%, 75%, 80%, 85%, 90%, and 95%. Sequence identity can be determined using, for example, the GAP, CLUSTALW, or BLAST programs.

As those of skill will appreciate, the present invention includes, but is not limited to, catalytically active polypeptides of the present invention (i.e., enzymes). Catalytically active polypeptides have a specific activity of at least 20%, 30%, or 40%, and preferably at least 50%, 60%, or 70%, and most preferably at least 80%, 90%, or 95% that of the native (non-synthetic), endogenous polypeptide. Further, the substrate specificity (k_{cat}/K_m) is optionally substantially similar to the native (non-synthetic), endogenous polypeptide. Typically, the K_m will be at least 30%, 40%, or 50%, that of the native (non-synthetic), endogenous polypeptide; and more preferably at least 60%, 70%, 80%, or 90%. Methods of

assaying and quantifying measures of enzymatic activity and substrate specificity (k_{cat}/K_m), are well known to those of skill in the art.

Expression of Proteins in Host Cells

Using the nucleic acids of the present invention, one may express a protein of the present invention in a recombinantly engineered cell such as bacteria, yeast, insect, mammalian, or preferably plant cells. The cells produce the protein in a non-natural condition (e.g., in quantity, composition, location, and/or time), because they have been genetically altered through human intervention to do so.

It is expected that those of skill in the art are knowledgeable in the numerous expression systems available for expression of a nucleic acid encoding a protein of the present invention. No attempt to describe in detail the various methods known for the expression of proteins in prokaryotes or eukaryotes will be made.

In brief summary, the expression of isolated nucleic acids encoding a protein of the present invention will typically be achieved by operably linking, for example, the DNA or cDNA to a promoter, followed by incorporation into an expression vector. The vector can be suitable for replication and integration in either prokaryotes or eukaryotes. Typical expression vectors contain transcription and translation terminators, initiation sequences, and promoters useful for regulation of the expression of the DNA encoding a protein of the present invention. To obtain high level expression of a cloned gene, it is desirable to construct expression vectors which contain, at the minimum, a strong promoter to direct transcription, a ribosome binding site for translational initiation, and a transcription/translation terminator. One of skill would recognize that modifications can be made to a protein of the present invention without diminishing its biological activity. Some modifications may be made to facilitate the cloning, expression, or incorporation of the targeting molecule into a fusion protein. Such modifications are well known to those of skill in the art and include, for example, a methionine added at the amino terminus to provide an initiation site, or additional amino acids (e.g., poly His) placed on either terminus to create conveniently located purification sequences. Restriction sites or termination codons can also be introduced.

Synthesis of Proteins

The proteins of the present invention can be constructed using non-cellular synthetic methods. Solid phase synthesis of proteins of less than about 50 amino acids in length may be accomplished by attaching the C-terminal amino acid of the sequence to an insoluble support followed by sequential addition of the remaining amino acids in the sequence. Techniques for solid phase synthesis are described by Barany and Merrifield, *Solid-Phase Peptide Synthesis*, pp. 3-284 in *The Peptides: Analysis, Synthesis, Biology. Vol. 2: Special Methods in Peptide Synthesis, Part A.*; Merrifield, et al., *J. Am. Chem. Soc.* 85: 2149-2156 (1963), and Stewart et al., *Solid Phase Peptide Synthesis*, 2nd ed., Pierce Chem. Co., Rockford, Ill. (1984). Proteins of greater length may be synthesized by condensation of the amino and carboxy termini of shorter fragments. Methods of forming peptide bonds by activation of a carboxy terminal end (e.g., by the use of the coupling reagent N,N'-dicyclohexylcarbodiimide) are known to those of skill.

Purification of Proteins

The proteins of the present invention may be purified by standard techniques well known to those of skill in the art.

Recombinantly produced proteins of the present invention can be directly expressed or expressed as a fusion protein. The recombinant protein is purified by a combination of cell lysis (e.g., sonication, French press) and affinity chromatography. For fusion products, subsequent digestion of the fusion protein with an appropriate proteolytic enzyme releases the desired recombinant protein.

The proteins of this invention, recombinant or synthetic, may be purified to substantial purity by standard techniques well known in the art, including detergent solubilization, selective precipitation with such substances as ammonium sulfate, column chromatography, immunopurification methods, and others. See, for instance, R. Scopes, *Protein Purification: Principles and Practice*, Springer-Verlag: New York (1982); Deutscher, *Guide to Protein Purification*, Academic Press (1990). For example, antibodies may be raised to the proteins as described herein. Purification from *E. coli* can be achieved following procedures described in U.S. Pat. No. 4,511,503. The protein may then be isolated from cells expressing the protein and further purified by standard protein chemistry techniques as described herein. Detection of the expressed protein is achieved by methods known in the art, including, for example, radioimmunoassays, Western blotting techniques or immunoprecipitation.

Introduction of Nucleic Acids Into Host Cells

The method of introducing a nucleic acid of the present invention into a host cell is not critical to the instant invention. Transformation or transfection methods are conveniently used. Accordingly, a wide variety of methods have been developed to insert a DNA sequence into the genome of a host cell to obtain the transcription and/or translation of the sequence to effect phenotypic changes in the organism. Thus, any method which provides for effective introduction of a nucleic acid may be employed.

A. Plant Transformation

A nucleic acid comprising a polynucleotide of the present invention is optionally introduced into a plant. Generally, the polynucleotide will first be incorporated into a recombinant expression cassette or vector. Isolated nucleic acid acids of the present invention can be introduced into plants according to techniques known in the art. Techniques for transforming a wide variety of higher plant species are well known and described in the technical, scientific, and patent literature. See, for example, Weising et al., *Ann. Rev. Genet.* 22: 421-477 (1988). For example, the DNA construct may be introduced directly into the genomic DNA of the plant cell using techniques such as electroporation, polyethylene glycol (PEG), poration, particle bombardment, silicon fiber delivery, or microinjection of plant cell protoplasts or embryogenic callus. See, e.g., Tomes, et al., *Direct DNA Transfer into Intact Plant Cells Via Microprojectile Bombardment*, pp. 197-213 in *Plant Cell, Tissue and Organ Culture, Fundamental Methods*, eds. O. L. Gamborg and G. C. Phillips. Springer-Verlag Berlin Heidelberg New York, 1995; see, U.S. Pat. No. 5,990,387. The introduction of DNA constructs using PEG precipitation is described in Paszkowski et al., *Embo J.* 3: 2717-2722 (1984). Electroporation techniques are described in Fromm et al., *Proc. Natl. Acad. Sci. (USA)* 82: 5824 (1985). Ballistic transformation techniques are described in Klein et al., *Nature* 327: 70-73 (1987).

Agrobacterium tumefaciens—mediated transformation techniques are well described in the scientific literature. See, for example Horsch et al., *Science* 233: 496-498 (1984); Fraley et al., *Proc. Natl. Acad. Sci. (USA)* 80: 4803 (1983); and, *Plant Molecular Biology: A Laboratory Manual*, Chap-

ter 8, Clark, Ed., Springer-Verlag, Berlin (1997). The DNA constructs may be combined with suitable T-DNA flanking regions and introduced into a conventional *Agrobacterium tumefaciens* host vector. The virulence functions of the *Agrobacterium tumefaciens* host will direct the insertion of the construct and adjacent marker into the plant cell DNA when the cell is infected by the bacteria. See, U.S. Pat. No. 5,591,616. Although *Agrobacterium* is useful primarily in dicots, certain monocots can be transformed by *Agrobacterium*. For instance, *Agrobacterium* transformation of maize is described in U.S. Pat. No. 5,550,318.

Other methods of transfection or transformation include (1) *Agrobacterium rhizogenes*—mediated transformation (see, e.g., Lichtenstein and Fuller In: *Genetic Engineering*, vol. 6, PWJ. Rigby, Ed., London, Academic Press, 1987; and Lichtenstein, C. P., and Draper, J. In: *DNA Cloning*, Vol. II, D. M. Glover, Ed., Oxford, IRI Press, 1985), Application PCT/US87/02512 (WO 88/02405 published Apr. 7, 1988) describes the use of *A. rhizogenes* strain A4 and its Ri plasmid along with *A. tumefaciens* vectors pARC8 or pARC16 (2) liposome-mediated DNA uptake (see, e.g., Freeman et al., *Plant Cell Physiol.* 25: 1353 (1984)), (3) the vortexing method (see, e.g., Kindle, *Proc. Natl. Acad. Sci., (USA)* 87: 1228 (1990).

DNA can also be introduced into plants by direct DNA transfer into pollen as described by Zhou et al., *Methods in Enzymology*, 101:433 (1983); D. Hess, *Intern Rev. Cytol.*, 107:367 (1987); Luo et al., *Plant Mol. Biol. Reporter*, 6:165 (1988). Expression of polypeptide coding genes can be obtained by injection of the DNA into reproductive organs of a plant as described by Pena et al., *Nature*, 325:274 (1987). DNA can also be injected directly into the cells of immature embryos and rehydrated desiccated embryos as described by Neuhaus et al., *Theor. Appl. Genet.*, 75:30 (1987); and Benbrook et al., in *Proceedings Bio Expo 1986*, Butterworth, Stoneham, Mass., pp. 27-54 (1986). A variety of plant viruses that can be employed as vectors are known in the art and include cauliflower mosaic virus (CaMV), geminivirus, brome mosaic virus, and tobacco mosaic virus.

B. Transfection of Prokaryotes, Lower Eukaryotes, and Animal Cells

Animal and lower eukaryotic (e.g., yeast) host cells are competent or rendered competent for transfection by various means. There are several well-known methods of introducing DNA into animal cells. These include: calcium phosphate precipitation, fusion of the recipient cells with bacterial protoplasts containing the DNA, treatment of the recipient cells with liposomes containing the DNA, DEAE dextran, electroporation, biolistics, and micro-injection of the DNA directly into the cells. The transfected cells are cultured by means well known in the art. Kuchler, R. J., *Biochemical Methods in Cell Culture and Virology*, Dowden, Hutchinson and Ross, Inc. (1977).

Transgenic Plant Regeneration

Plant cells which directly result or are derived from the nucleic acid introduction techniques can be cultured to regenerate a whole plant which possesses the introduced genotype. Such regeneration techniques often rely on manipulation of certain phytohormones in a tissue culture growth medium. Plants cells can be regenerated, e.g., from single cells, callus tissue or leaf discs according to standard plant tissue culture techniques. It is well known in the art that various cells, tissues, and organs from almost any plant can be successfully cultured to regenerate an entire plant. Plant regeneration from cultured protoplasts is described in Evans et al., *Protoplasts Isolation and Culture, Handbook of*

Plant Cell Culture, Macmillan Publishing Company, New York, pp. 124-176 (1983); and Binding, *Regeneration of Plants, Plant Protoplasts*, CRC Press, Boca Raton, pp. 21-73 (1985).

The regeneration of plants from either single plant protoplasts or various explants is well known in the art. See, for example, *Methods for Plant Molecular Biology*, A. Weissbach and H. Weissbach, eds., Academic Press, Inc., San Diego, Calif. (1988). This regeneration and growth process includes the steps of selection of transformant cells and shoots, rooting the transformant shoots and growth of the plantlets in soil. For maize cell culture and regeneration see generally, *The Maize Handbook*, Freeling and Walbot, Eds., Springer, New York (1994); *Corn and Corn Improvement*, 3rd edition, Sprague and Dudley Eds., American Society of Agronomy, Madison, Wis. (1988). For transformation and regeneration of maize see, Gordon-Kamm et al., *The Plant Cell*, 2:603-618 (1990).

The regeneration of plants containing the polynucleotide of the present invention and introduced by *Agrobacterium* from leaf explants can be achieved as described by Horsch et al., *Science*, 227:1229-1231 (1985). In this procedure, transformants are grown in the presence of a selection agent and in a medium that induces the regeneration of shoots in the plant species being transformed as described by Fraley et al., *Proc. Natl. Acad. Sci. (U.S.A.)*, 80:4803 (1983). This procedure typically produces shoots within two to four weeks and these transformant shoots are then transferred to an appropriate root-inducing medium containing the selective agent and an antibiotic to prevent bacterial growth. Transgenic plants of the present invention may be fertile or sterile.

One of skill will recognize that after the recombinant expression cassette is stably incorporated in transgenic plants and confirmed to be operable, it can be introduced into other plants by sexual crossing. Any of a number of standard breeding techniques can be used, depending upon the species to be crossed. In vegetatively propagated crops, mature transgenic plants can be propagated by the taking of cuttings or by tissue culture techniques to produce multiple identical plants. Selection of desirable transgenics is made and new varieties are obtained and propagated vegetatively for commercial use. In seed propagated crops, mature transgenic plants can be self crossed to produce a homozygous inbred plant. The inbred plant produces seed containing the newly introduced nucleic acid. These seeds can be grown to produce plants with the selected phenotype. Parts obtained from the regenerated plant, such as flowers, seeds, leaves, branches, fruit, and the like are included in the invention, provided that these parts comprise cells comprising the isolated nucleic acid of the present invention. Progeny, variants, and mutants of the regenerated plants are also included within the scope of the invention, provided that these parts comprise the introduced nucleic acid sequences. Transgenic plants expressing a polynucleotide of the present invention can be screened for transmission of the nucleic acid of the present invention by, for example, standard immunoblot and DNA detection techniques. Expression at the RNA level can be determined initially to identify and quantitate expression-positive plants. Standard techniques for RNA analysis can be employed and include PCR amplification assays using oligonucleotide primers designed to amplify only the heterologous RNA templates and solution hybridization assays using heterologous nucleic acid-specific probes. The RNA-positive plants can then be analyzed for protein expression by Western immunoblot analysis using the specifically reactive antibodies of the present

invention. In addition, in situ hybridization and immunocytochemistry according to standard protocols can be done using heterologous nucleic acid specific polynucleotide probes and antibodies, respectively, to localize sites of expression within transgenic tissue. Generally, a number of transgenic lines are usually screened for the incorporated nucleic acid to identify and select plants with the most appropriate expression profiles.

A preferred embodiment is a transgenic plant that is homozygous for the added heterologous nucleic acid; i.e., a transgenic plant that contains two added nucleic acid sequences, one gene at the same locus on each chromosome of a chromosome pair. A homozygous transgenic plant can be obtained by sexually mating (selfing) a heterozygous transgenic plant that contains a single added heterologous nucleic acid, germinating some of the seed produced and analyzing the resulting plants for altered expression of a polynucleotide of the present invention relative to a control plant (i.e., native, non-transgenic). Back-crossing to a parental plant and out-crossing with a non-transgenic plant are also contemplated.

Modulating Polypeptide Levels and/or Composition

The present invention further provides a method for modulating (i.e., increasing or decreasing) the concentration or ratio of the polypeptides of the present invention in a plant or part thereof. Modulation can be effected by increasing or decreasing the concentration and/or the ratio of the polypeptides of the present invention in a plant. The method comprises introducing into a plant cell a recombinant expression cassette comprising a polynucleotide of the present invention as described above to obtain a transgenic plant cell, culturing the transgenic plant cell under transgenic plant cell growing conditions, and inducing or repressing expression of a polynucleotide of the present invention in the transgenic plant for a time sufficient to modulate concentration and/or the ratios of the polypeptides in the transgenic plant or plant part.

In some embodiments, the concentration and/or ratios of polypeptides of the present invention in a plant may be modulated by altering, in vivo or in vitro, the promoter of a gene to up- or down-regulate gene expression. In some embodiments, the coding regions of native genes of the present invention can be altered via substitution, addition, insertion, or deletion to decrease activity of the encoded enzyme. See, e.g., Kmiec, U.S. Pat. No. 5,565,350; Zarling et al., PCT/US93/03868. And in some embodiments, an isolated nucleic acid (e.g., a vector) comprising a promoter sequence is transfected into a plant cell. Subsequently, a plant cell comprising the promoter operably linked to a polynucleotide of the present invention is selected for by means known to those of skill in the art such as, but not limited to, Southern blot, DNA sequencing, or PCR analysis using primers specific to the promoter and to the gene and detecting amplicons produced therefrom. A plant or plant part altered or modified by the foregoing embodiments is grown under plant-forming conditions for a time sufficient to modulate the concentration and/or ratios of polypeptides of the present invention in the plant. Plant-forming conditions are well known in the art and discussed briefly, supra.

In general, concentration or the ratios of the polypeptides is increased or decreased by at least 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, or 90% relative to a native control plant, plant part, or cell lacking the aforementioned recombinant expression cassette. Modulation in the present invention may occur during and/or subsequent to growth of the plant to the desired stage of development. Modulating

nucleic acid expression temporally and/or in particular tissues can be controlled by employing the appropriate promoter operably linked to a polynucleotide of the present invention in, for example, sense or antisense orientation as discussed in greater detail, supra. Induction of expression of a polynucleotide of the present invention can also be controlled by exogenous administration of an effective amount of inducing compound. Inducible promoters and inducing compounds which activate expression from these promoters are well known in the art. In preferred embodiments, the polypeptides of the present invention are modulated in monocots, particularly maize.

UTRs and Codon Preference

In general, translational efficiency has been found to be regulated by specific sequence elements in the 5' non-coding or untranslated region (5' UTR) of the RNA. Positive sequence motifs include translational initiation consensus sequences (Kozak, *Nucleic Acids Res.* 15:8125 (1987)) and the 7-methylguanosine cap structure (Drummond et al., *Nucleic Acids Res.* 13:7375 (1985)). Negative elements include stable intramolecular 5' UTR stem-loop structures (Muesing et al., *Cell* 48:691 (1987)) and AUG sequences or short open reading frames preceded by an appropriate AUG in the 5' UTR (Kozak, supra, Rao et al., *Mol. and Cell. Biol.* 8:284 (1988)). Accordingly, the present invention provides 5' and/or 3' untranslated regions for modulation of translation of heterologous coding sequences.

Further, the polypeptide-encoding segments of the polynucleotides of the present invention can be modified to alter codon usage. Altered codon usage can be employed to alter translational efficiency and/or to optimize the coding sequence for expression in a desired host such as to optimize the codon usage in a heterologous sequence for expression in maize. Codon usage in the coding regions of the polynucleotides of the present invention can be analyzed statistically using commercially available software packages such as "Codon Preference" available from the University of Wisconsin Genetics Computer Group (see Devereaux et al., *Nucleic Acids Res.* 12: 387-395 (1984)) or MacVector 4.1 (Eastman Kodak Co., New Haven, Conn.). Thus, the present invention provides a codon usage frequency characteristic of the coding region of at least one of the polynucleotides of the present invention. The number of polynucleotides that can be used to determine a codon usage frequency can be any integer from 1 to the number of polynucleotides of the present invention as provided herein. Optionally, the polynucleotides will be full-length sequences. An exemplary number of sequences for statistical analysis can be at least 1, 5, 10, 20, 50, or 100.

Sequence Shuffling

The present invention provides methods for sequence shuffling using polynucleotides of the present invention, and compositions resulting therefrom. Sequence shuffling is described in PCT publication No. WO 97/20078. See also, Zhang, J.-H., et al., *Proc. Natl. Acad. Sci. USA* 94:4504-4509 (1997). Generally, sequence shuffling provides a means for generating libraries of polynucleotides having a desired characteristic which can be selected or screened for. Libraries of recombinant polynucleotides are generated from a population of related sequence polynucleotides which comprise sequence regions which have substantial sequence identity and can be homologously recombined in vitro or in vivo. The population of sequence-recombined polynucleotides comprises a subpopulation of polynucleotides which possess desired or advantageous characteristics and which can be selected by a suitable selection or screen-

ing method. The characteristics can be any property or attribute capable of being selected for or detected in a screening system, and may include properties of: an encoded protein, a transcriptional element, a sequence controlling transcription, RNA processing, RNA stability, chromatin conformation, translation, or other expression property of a gene or transgene, a replicative element, a protein-binding element, or the like, such as any feature which confers a selectable or detectable property. In some embodiments, the selected characteristic will be a decreased K_m and/or increased K_{cat} over the wild-type protein as provided herein. In other embodiments, a protein or polynucleotide generated from sequence shuffling will have a ligand binding affinity greater than the non-shuffled wild-type polynucleotide. The increase in such properties can be at least 110%, 120%, 130%, 140% or at least 150% of the wild-type value.

Generic and Consensus Sequences

Polynucleotides and polypeptides of the present invention further include those having:

- (a) a generic sequence of at least two homologous polynucleotides or polypeptides, respectively, of the present invention; and, (b) a consensus sequence of at least three homologous polynucleotides or polypeptides, respectively, of the present invention. The generic sequence of the present invention comprises each species of polypeptide or polynucleotide embraced by the generic polypeptide or polynucleotide sequence, respectively. The individual species encompassed by a polynucleotide having an amino acid or nucleic acid consensus sequence can be used to generate antibodies or produce nucleic acid probes or primers to screen for homologs in other species, genera, families, orders, classes, phyla, or kingdoms. For example, a polynucleotide having a consensus sequence from a gene family of *Zea mays* can be used to generate antibody or nucleic acid probes or primers to other Gramineae species such as wheat, rice, or sorghum. Alternatively, a polynucleotide having a consensus sequence generated from orthologous genes can be used to identify or isolate orthologs of other taxa. Typically, a polynucleotide having a consensus sequence will be at least 9, 10, 15, 20, 25, 30, or 40 amino acids in length, or 20, 30, 40, 50, 100, or 150 nucleotides in length. As those of skill in the art are aware, a conservative amino acid substitution can be used for amino acids which differ amongst aligned sequences but are from the same conservative substitution group as discussed above. Optionally, no more than 1 or 2 conservative amino acids are substituted for each 10 amino acid length of consensus sequence.

Similar sequences used for generation of a consensus or generic sequence include any number and combination of allelic variants of the same gene, orthologous, or paralogous sequences as provided herein. Optionally, similar sequences used in generating a consensus or generic sequence are identified using the BLAST program's smallest sum probability (P(N)). Various suppliers of sequence-analysis software are listed in chapter 7 of *Current Protocols in Molecular Biology*, F. M. Ausubel et al., Eds., Current Protocols, a joint venture between Greene Publishing Associates, Inc. and John Wiley & Sons, Inc. (Supplement 30). A polynucleotide sequence is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.1, more preferably less than about 0.01, or 0.001, and most preferably less than about 0.0001, or 0.00001. Similar polynucleotides can be aligned and a consensus or generic

sequence generated using multiple sequence alignment software available from a number of commercial suppliers such as the Genetics Computer Group's (Madison, Wis.) PILEUP software, Vector NTI's (North Bethesda, Md.) ALIGNX, or Genecode's (Ann Arbor, Mich.) SEQUENCHER. Conveniently, default parameters of such software can be used to generate consensus or generic sequences.

Detection of Nucleic Acids

The present invention further provides methods for detecting a polynucleotide of the present invention in a nucleic acid sample suspected of containing a polynucleotide of the present invention, such as a plant cell lysate, particularly a lysate of maize. In some embodiments, a cognate gene of a polynucleotide of the present invention or portion thereof can be amplified prior to the step of contacting the nucleic acid sample with a polynucleotide of the present invention. The nucleic acid sample is contacted with the polynucleotide to form a hybridization complex. The polynucleotide hybridizes under stringent conditions to a gene encoding a polypeptide of the present invention. Formation of the hybridization complex is used to detect a gene encoding a polypeptide of the present invention in the nucleic acid sample. Those of skill will appreciate that an isolated nucleic acid comprising a polynucleotide of the present invention should lack cross-hybridizing sequences in common with non-target genes that would yield a false positive result. Detection of the hybridization complex can be achieved using any number of well-known methods. For example, the nucleic acid sample, or a portion thereof, may be assayed by hybridization formats including but not limited to, solution phase, solid phase, mixed phase, or in situ hybridization assays.

Detectable labels suitable for use in the present invention include any composition detectable by spectroscopic, radioisotopic, photochemical, biochemical, immunochemical, electrical, optical or chemical means. Useful labels in the present invention include biotin for staining with labeled streptavidin conjugate, magnetic beads, fluorescent dyes, radiolabels, enzymes, and calorimetric labels. Other labels include ligands which bind to antibodies labeled with fluorophores, chemiluminescent agents, and enzymes. Labeling the nucleic acids of the present invention is readily achieved such as by the use of labeled PCR primers.

In certain embodiments the nucleic acid sequences of the present invention can be used in combination ("stacked") with other polynucleotide sequences of interest in order to create plants with a desired phenotype. The combinations generated can include multiple copies of any one or more of the polynucleotides of interest. The polynucleotides of the present invention may be stacked with any gene or combination of genes to produce plants with a variety of desired trait combinations, including but not limited to traits desirable for animal feed such as high oil genes (e.g., U.S. Pat. No. 6,232,529); balanced amino acids (e.g. hordothionins (U.S. Pat. Nos. 5,990,389; 5,885,801; 5,885,802; and 5,703,409); barley high lysine (Williamson et al., (1987) *Eur. J. Biochem.* 165:99-106; and WO 98/20122); and high methionine proteins (Pedersen et al., (1986) *J. Biol. Chem.* 261:6279; Kirihara et al. (1988) *Gene* 71:359; and Musumura et al., (1989) *Plant Mol. Biol.* 12: 123)); increased digestibility (e.g., modified storage proteins (U.S. application Ser. No. 10/053,410, filed Nov. 7, 2001); and thioredoxins (U.S. application Ser. No. 10/005,429, filed Dec. 3, 2001)), the disclosures of which are herein incorporated by reference. The polynucleotides of the present invention can also be stacked with traits desirable for insect,

disease or herbicide resistance (e.g., *Bacillus thuringiensis* toxic proteins (U.S. Pat. Nos. 5,366,892; 5,747,450; 5,737,514; 5,723,756; 5,593,881; Geiser et al., (1986) *Gene* 48:109); lectins (Van Damme et al., (1994) *Plant Mol. Biol.* 24:825); fumonisin detoxification genes (U.S. Pat. No. 5,792,931); avirulence and disease resistance genes (Jones et al., (1994) *Science* 266:789; Martin et al., (1993) *Science* 262:1432; Mindrinos et al., (1994) *Cell* 78:1089); acetolactate synthase (ALS) mutants that lead to herbicide resistance such as the S4 and/or Hra mutations; inhibitors of glutamine synthase such as phosphinothricin or basta (e.g., bar gene); and glyphosate resistance (EPSPS gene)); and traits desirable for processing or process products such as high oil (e.g., U.S. Pat. No. 6,232,529); modified oils (e.g., fatty acid desaturase genes (U.S. Pat. No. 5,952,544; WO 94/11516)); modified starches (e.g., ADPG pyrophosphorylases (AG-Pase), starch synthases (SS), starch branching enzymes (SBE) and starch debranching enzymes (SDBE)); and polymers or bioplastics (e.g., U.S. Pat. No. 5,602,321; beta-ketothiolase, polyhydroxybutyrate synthase, and acetoacetyl-CoA reductase (Schubert et al., (1988) *J. Bacteriol.* 170:5837-5847) facilitate expression of polyhydroxyalkanoates (PHAs)), the disclosures of which are herein incorporated by reference. One could also combine the polynucleotides of the present invention with polynucleotides affecting agronomic traits such as male sterility (e.g., see U.S. Pat. No. 5,583,210), stalk strength, flowering time, or transformation technology traits such as cell cycle regulation or gene targeting (e.g. WO 99/61619; WO 00/17364; WO 99/25821), the disclosures of which are herein incorporated by reference.

These stacked combinations can be created by any method, including but not limited to cross breeding plants by any conventional or TopCross methodology, or genetic transformation. If the traits are stacked by genetically transforming the plants, the polynucleotide sequences of interest can be combined at any time and in any order. For example, a transgenic plant comprising one or more desired traits can be used as the target to introduce further traits by subsequent transformation. The traits can be introduced simultaneously in a co-transformation protocol with the polynucleotides of interest provided by any combination of transformation cassettes. For example, if two sequences will be introduced, the two sequences can be contained in separate transformation cassettes (trans) or contained on the same transformation cassette (cis). Expression of the sequences of interest can be driven by the same promoter or by different promoters. In certain cases, it may be desirable to introduce a transformation cassette that will suppress the expression of a polynucleotide of interest. This may be accompanied by any combination of other suppression cassettes or overexpression cassettes to generate the desired combination of traits in the plant.

The transformed plants of the invention may be used in a plant breeding program. The goal of plant breeding is to combine, in a single variety or hybrid, various desirable traits. For field crops, these traits may include, for example, resistance to diseases and insects, tolerance to heat and drought, reduced time to crop maturity, greater yield, and better agronomic quality. With mechanical harvesting of many crops, uniformity of plant characteristics such as germination and stand establishment, growth rate, maturity, and plant and ear height, is desirable. Traditional plant breeding is an important tool in developing new and improved commercial crops. This invention encompasses methods for producing a maize plant by crossing a first parent maize plant with a second parent maize plant wherein

one or both of the parent maize plants is a transformed plant displaying enhanced vigor, as described herein.

Plant breeding techniques known in the art and used in a maize plant breeding program include, but are not limited to, recurrent selection, bulk selection, mass selection, backcrossing, pedigree breeding, open pollination breeding, restriction fragment length polymorphism enhanced selection, genetic marker enhanced selection, doubled haploids, and transformation. Often combinations of these techniques are used.

The development of maize hybrids in a maize plant breeding program requires, in general, the development of homozygous inbred lines, the crossing of these lines, and the evaluation of the crosses. There are many analytical methods available to evaluate the result of a cross. The oldest and most traditional method of analysis is the observation of phenotypic traits. Alternatively, the genotype of a plant can be examined.

A genetic trait which has been engineered into a particular maize plant using transformation techniques, could be moved into another line using traditional breeding techniques that are well known in the plant breeding arts. For example, a backcrossing approach is commonly used to move a transgene from a transformed maize plant to an elite inbred line, and the resulting progeny would then comprise the transgene(s). Also, if an inbred line was used for the transformation then the transgenic plants could be crossed to a different inbred in order to produce a transgenic hybrid maize plant. As used herein, "crossing" can refer to a simple X by Y cross, or the process of backcrossing, depending on the context.

The development of a maize hybrid in a maize plant breeding program involves three steps: (1) the selection of plants from various germplasm pools for initial breeding crosses; (2) the selfing of the selected plants from the breeding crosses for several generations to produce a series of inbred lines, which, while different from each other, breed true and are highly uniform; and (3) crossing the selected inbred lines with different inbred lines to produce the hybrids. During the inbreeding process in maize, the vigor of the lines decreases. Vigor is restored when two different inbred lines are crossed to produce the hybrid. An important consequence of the homozygosity and homogeneity of the inbred lines is that the hybrid created by crossing a defined pair of inbreds will always be the same. Once the inbreds that give a superior hybrid have been identified, the hybrid seed can be reproduced indefinitely as long as the homogeneity of the inbred parents is maintained.

Transgenic plants of the present invention may be used to produce a single cross hybrid, a three-way hybrid or a double cross hybrid. A single cross hybrid is produced when two inbred lines are crossed to produce the F1 progeny. A double cross hybrid is produced from four inbred lines crossed in pairs (A×B and C×D) and then the two F1 hybrids are crossed again (A×B)×(C×D). A three-way cross hybrid is produced from three inbred lines where two of the inbred lines are crossed (A×B) and then the resulting F1 hybrid is crossed with the third inbred (A×B)×C. Much of the hybrid vigor and uniformity exhibited by F1 hybrids is lost in the next generation (F2). Consequently, seed produced by hybrids is consumed rather than planted.

Although the present invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be obvious that certain changes and modifications may be practiced within the scope of the appended claims.

This example describes the construction of a cDNA library.

Total RNA can be isolated from maize tissues with TRIzol Reagent (Life Technology Inc. Gaithersburg, Md.) using a modification of the guanidine isothiocyanate/acid-phenol procedure described by Chomczynski and Sacchi (Chomczynski, P., and Sacchi, N. *Anal. Biochem.* 162, 156 (1987)). In brief, plant tissue samples are pulverized in liquid nitrogen before the addition of the TRIzol Reagent, and then further homogenized with a mortar and pestle. Addition of chloroform followed by centrifugation is conducted for separation of an aqueous phase and an organic phase. The total RNA is recovered by precipitation with isopropyl alcohol from the aqueous phase.

The selection of poly(A)+RNA from total RNA can be performed using PolyATact system (Promega Corporation, Madison, Wis.). Biotinylated oligo(dT) primers are used to hybridize to the 3' poly(A) tails on mRNA. The hybrids are captured using streptavidin coupled to paramagnetic particles and a magnetic separation stand. The mRNA is then washed at high stringency conditions and eluted by RNase-free deionized water.

cDNA synthesis and construction of unidirectional cDNA libraries can be accomplished using the SuperScript Plasmid System (Life Technology Inc. Gaithersburg, Md.). The first strand of cDNA is synthesized by priming an oligo(dT) primer containing a Not I site. The reaction is catalyzed by SuperScript Reverse Transcriptase II at 45° C. The second strand of cDNA is labeled with alpha-³²P-dCTP and a portion of the reaction analyzed by agarose gel electrophoresis to determine cDNA sizes. cDNA molecules smaller than 500 base pairs and unligated adapters are removed by Sephacryl-S400 chromatography. The selected cDNA molecules are ligated into pSPORT1 vector in between of Not I and Sal I sites.

Alternatively, cDNA libraries can be prepared by any one of many methods available. For example, the cDNAs may be introduced into plasmid vectors by first preparing the cDNA libraries in Uni-ZAP™ XR vectors according to the manufacturer's protocol (Stratagene Cloning Systems, La Jolla, Calif.). The Uni-ZAP™ XR libraries are converted into plasmid libraries according to the protocol provided by Stratagene. Upon conversion, cDNA inserts will be contained in the plasmid vector pBluescript. In addition, the cDNAs may be introduced directly into pre-cut Bluescript II SK(+) vectors (Stratagene) using T4 DNA ligase (New England Biolabs), followed by transfection into DH10B cells according to the manufacturer's protocol (GIBCO BRL Products). Once the cDNA inserts are in plasmid vectors, plasmid DNAs are prepared from randomly picked bacterial colonies containing recombinant pBluescript plasmids, or the insert cDNA sequences are amplified via polymerase chain reaction using primers specific for vector sequences flanking the inserted cDNA sequences. Amplified insert DNAs or plasmid DNAs are sequenced in dye-primer sequencing reactions to generate partial cDNA sequences (expressed sequence tags or "ESTs"; see Adams et al., (1991) *Science* 252:1651-1656). The resulting ESTs are analyzed using a Perkin Elmer Model 377 fluorescent sequencer.

This method describes construction of a full-length enriched cDNA library.

An enriched full-length cDNA library can be constructed using one of two variations of the method of Carninci et al., *Genomics* 37: 327-336, 1996. These variations are based on chemical introduction of a biotin group into the diol residue of the 5' cap structure of eukaryotic mRNA to select full-length first strand cDNA. The selection occurs by trapping the biotin residue at the cap sites using streptavidin-coated magnetic beads followed by RNase I treatment to eliminate incompletely synthesized cDNAs. Second strand cDNA is synthesized using established procedures such as those provided in Life Technologies' (Rockville, Md.) "SuperScript Plasmid System for cDNA Synthesis and Plasmid Cloning" kit. Libraries made by this method have been shown to contain 50% to 70% full-length cDNAs.

The first strand synthesis methods are detailed below. An asterisk denotes that the reagent was obtained from Life Technologies, Inc.

A. First Strand cDNA Synthesis Method 1 (with Trehalose)

mRNA (10 ug)	25 μ l
*Not I primer (5 ug)	10 μ l
*5x 1 st strand buffer	43 μ l
*0.1 m DTT	20 μ l
*dNTP mix 10 mm	10 μ l
BSA 10 ug/ μ l	1 μ l
Trehalose (saturated)	59.2 μ l
RNase inhibitor (Promega)	1.8 μ l
*Superscript II RT 200 u/ μ l	20 μ l
100% glycerol	18 μ l
Water	7 μ l

The mRNA and Not I primer are mixed and denatured at 65° C. for 10 min. They are then chilled on ice and other components added to the tube. Incubation is at 45° C. for 2 min. Twenty microliters of RT (reverse transcriptase) is added to the reaction and start program on the thermocycler (MJ. Research, Waltham, Mass.):

Step 1	45° C. 10 min
Step 2	45° C. -0.3° C./cycle, 2 seconds/cycle
Step 3	go to 2 for 33 cycles
Step 4	35° C. 5 min
Step 5	45° C. 5 min
Step 6	45° C. 0.2° C./cycle, 1 sec/cycle
Step 7	go to 7 for 49 cycles
Step 8	55° C. 0.1° C./cycle, 12 sec/cycle
Step 9	go to 8 for 49 cycles
Step 10	55° C. 2 min
Step 11	60° C. 2 min
Step 12	go to 11 for 9 times
Step 13	4° C. forever
Step 14	end

B. First Strand cDNA Synthesis Method 2

mRNA (10 μ g)	25 μ l
water	30 μ l
*Not I adapter primer (5 μ g)	10 μ l

65° C. for 10 min, chill on ice, then add following reagents,

-continued

*5x first buffer	20 μ l
*0.1 M DTT	10 μ l
*10 mM dNTP mix	5 μ l

Incubate at 45° C. for 2 min, then add 10 μ l of *SuperScript II RT (200 u/ μ l), start the following program:

Step 1	45° C. for 6 sec, -0.1° C./cycle
Step 2	go to 1 for 99 additional cycles
Step 3	35° C. for 5 min
Step 4	45° C. for 60 min
Step 5	50° C. for 10 min
Step 6	4° C. forever
Step 7	end

After the 1st strand cDNA synthesis, the DNA is extracted by phenol according to standard procedures, and then precipitated in NaOAc and ethanol, and stored in -20° C.

C. Oxidization of the Diol Group of mRNA for Biotin Labeling

First strand cDNA is spun down and washed once with 70% EtOH. The pellet is resuspended in 23.2 μ l of DEPC treated water and put on ice. Prepare 100 mM of NaIO₄ freshly, and then add the following reagents:

mRNA: 1 st cDNA (start with 20 μ g mRNA)	46.4 μ l
100 mM NaIO ₄ (freshly made)	2.5 μ l
NaOAc 3 M pH 4.5	1.1 μ l

To make 100 mM NaIO₄, use 21.39 μ g of NaIO₄ for 1 μ l of water.

Wrap the tube in a foil and incubate on ice for 45 min.

After the incubation, the reaction is then precipitated in:

5 M NaCl	10 μ l
20% SDS	0.5 μ l
isopropanol	61 μ l

Incubate on ice for at least 30 min, then spin it down at max speed at 4° C. for 30 min and wash once with 70% ethanol and then 80% EtOH.

D. Biotinylation of the mRNA Diol Group

Resuspend the DNA in 110 μ l DEPC treated water, then add the following reagents:

20% SDS	5 μ l
2 M NaOAc pH 6.1	5 μ l
10 mm biotin hydrazide (freshly made)	300 μ l

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Wrap in a foil and incubate at room temperature overnight.

E. RNase I Treatment

Precipitate DNA in:

5 M NaCl	10 μ l
2 M NaOAc pH 6.1	75 μ l
biotinylated mRNA:cDNA	420 μ l
100% EtOH (2.5 Vol)	1262.5 μ l

(Perform this precipitation in two tubes and split the 420 μ l of DNA into 210 μ l each, add 5 μ l of 5M NaCl, 37.5 μ l of 2M NaOAc pH 6.1, and 631.25 μ l of 100% EtOH).

Store at -20° C. for at least 30 min. Spin the DNA down at 4° C. at maximal speed for 30 min. and wash with 80% EtOH twice, then dissolve DNA in 70 μ l RNase free water. Pool two tubes and end up with 140 μ l.

Add the following reagents:

RNase One 10 U/ μ l	40 μ l
1 st cDNA:RNA	140 μ l
10X buffer	20 μ l

Incubate at 37° C. for 15 min.

Add 5 μ l of 40 μ g/ μ l yeast tRNA to each sample for capturing.

F. Full Length 1st cDNA Capturing

Blocking the beads with yeast tRNA:

Beads	1 ml
Yeast tRNA 40 μ g/ μ l	5 μ l

Incubate on ice for 30 min with mixing, wash 3 times with 1 ml of 2M NaCl, 50 mM EDTA, pH 8.0.

Resuspend the beads in 800 μ l of 2M NaCl, 50 mM EDTA, pH 8.0, add RNase I treated sample 200 μ l, and incubate the reaction for 30 min at room temperature. Capture the beads using the magnetic stand, save the supernatant, and start following washes:

2 washes with 2M NaCl, 50 mM EDTA, pH 8.0, 1 ml each time,

1 wash with 0.4% SDS, 50 μ g/ml tRNA,

1 wash with 10 mM Tris-Cl pH 7.5, 0.2 mM EDTA, 10 mM NaCl, 20% glycerol,

1 wash with 50 μ g/ml tRNA,

1 wash with 1st cDNA buffer

G. Second Strand cDNA Synthesis

Resuspend the beads in:

*5X first buffer	8 μ l
*0.1 mM DTT	4 μ l
*10 mM dNTP mix	8 μ l
*5X 2nd buffer	60 μ l
* <i>E. coli</i> Ligase 10 U/ μ l	2 μ l
* <i>E. coli</i> DNA polymerase 10 U/ μ l	8 μ l
* <i>E. coli</i> RNaseH 2 U/ μ l	2 μ l

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-continued

P32 dCTP 10 μ ci/ μ l	2 μ l
Or water up to 300 μ l	208 μ l

Incubate at 16° C. for 2 hr with mixing the reaction in every 30 min. Add 4 μ l of T4 DNA polymerase and incubate for additional 5 min at 16° C.

Elute 2nd cDNA from the beads.

Use a magnetic stand to separate the 2nd cDNA from the beads, then resuspend the beads in 200 μ l of water, and then separate again, pool the samples (about 500 μ l),

Add 200 μ l of water to the beads, then 200 μ l of phenol: chloroform, vortex, and spin to separate the sample with phenol.

Pool the DNA together (about 700 μ l) and use phenol to clean the DNA again, DNA is then precipitated in 2 μ g of glycogen and 0.5 vol of 7.5M NH₄OAc and 2 vol of 100% EtOH.

Precipitate overnight. Spin down the pellet and wash with 70% EtOH, air-dry the pellet.

DNA	250 μ l	DNA	200 μ l
7.5M NH ₄ OAc	125 μ l	7.5M NH ₄ OAc	100 μ l
100% EtOH	750 μ l	100% EtOH	600 μ l
glycogen 1 μ g/ μ l	2 μ l	glycogen 1 μ g/ μ l	2 μ l

H. Sal I Adapter Ligation

Resuspend the pellet in 26 μ l of water and use 1 μ l for TAE gel.

Set up reaction as following:

2 nd strand cDNA	25 μ l
*5X T4 DNA ligase buffer	10 μ l
*Sal I adapters	10 μ l
*T4 DNA ligase	5 μ l

Mix gently, incubate the reaction at 16° C. overnight.

Add 2 μ l of ligase second day and incubate at room temperature for 2 hrs (optional).

Add 50 μ l water to the reaction and use 100 μ l of phenol to clean the DNA, 90 μ l of the upper phase is transferred into a new tube and precipitate in:

Glycogen 1 μ g/ μ l	2 μ l
Upper phase DNA	90 μ l
7.5M NH ₄ OAc	50 μ l
100% EtOH	300 μ l

precipitate at -20° C. overnight

Spin down the pellet at 4° C. and wash in 70% EtOH, dry the pellet.

I. Not I Digestion

2 nd cDNA	41 μ l
*Reaction 3 buffer	5 μ l
*Not I 15 u/ μ l	4 μ l

Mix gently and incubate the reaction at 37° C. for 2 hr. Add 50 µl of water and 100 µl of phenol, vortex, and take 90 µl of the upper phase to a new tube, then add 50 µl of NH₄OAc and 300 µl of EtOH. Precipitate overnight at -20° C.

Cloning, ligation, and transformation are performed per the Superscript cDNA synthesis kit.

EXAMPLE 3

This example describes cDNA sequencing and library subtraction.

Individual colonies can be picked and DNA prepared either by PCR with M13 forward primers and M13 reverse primers, or by plasmid isolation. cDNA clones can be sequenced using M13 reverse primers.

cDNA libraries are plated out on 22×22 cm² agar plate at density of about 3,000 colonies per plate. The plates are incubated in a 37° C. incubator for 12-24 hours. Colonies are picked into 384-well plates by a robot colony picker, Q-bot (GENETIX Limited). These plates are incubated overnight at 37° C. Once sufficient colonies are picked, they are pinned onto 22×22 cm² nylon membranes using Q-bot. Each membrane holds 9,216 or 36,864 colonies. These membranes are placed onto an agar plate with an appropriate antibiotic. The plates are incubated at 37° C. overnight.

After colonies are recovered on the second day, these filters are placed on filter paper prewetted with denaturing solution for four minutes, then incubated on top of a boiling water bath for an additional four minutes. The filters are then placed on filter paper prewetted with neutralizing solution for four minutes. After excess solution is removed by placing the filters on dry filter papers for one minute, the colony side of the filters is placed into Proteinase K solution, incubated at 37° C. for 40-50 minutes. The filters are placed on dry filter papers to dry overnight. DNA is then cross-linked to nylon membrane by UV light treatment.

Colony hybridization is conducted as described by Sambrook, J., Fritsch, E. F. and Maniatis, T., (in *Molecular Cloning: A laboratory Manual*, 2nd Edition). The following probes can be used in colony hybridization:

1. First strand cDNA from the same tissue as the library was made from to remove the most redundant clones.
2. 48-192 most redundant cDNA clones from the same library based on previous sequencing data.
3. 192 most redundant cDNA clones in the entire maize sequence database.
4. A Sal-A20 oligo nucleotide: TCG ACC CAC GCG TCC GAA AAA AAA AAA AAA AAA AAA, removes clones containing a poly A tail but no cDNA.
5. cDNA clones derived from rRNA.

The image of the autoradiography is scanned into computer and the signal intensity and cold colony addresses of each colony is analyzed. Re-arranging of cold-colonies from 384 well plates to 96 well plates is conducted using Q-bot.

EXAMPLE 4

This example describes identification of the gene from a computer homology search.

Gene identities can be determined by conducting BLAST (Basic Local Alignment Search Tool; Altschul, S. F., et al., (1993) *J. Mol. Biol.* 215:403-410; see also www.ncbi.nlm.nih.gov/BLAST/) searches under default parameters for similarity to sequences contained in the BLAST "nr" database (comprising all non-redundant GenBank CDS translations, sequences derived from the 3-dimensional structure

Brookhaven Protein Data Bank, the last major release of the SWISS-PROT protein sequence database, EMBL, and DDBJ. databases). The cDNA sequences are analyzed for similarity to all publicly available DNA sequences contained in the "nr" database using the BLASTN program. The DNA sequences are translated in all reading frames and compared for similarity to all publicly available protein sequences contained in the "nr" database using the BLASTX program (Gish, W. and States, D. J. *Nature Genetics* 3:266-272 (1993)) provided by the NCBI. In some cases, the sequencing data from two or more clones containing overlapping segments of DNA are used to construct contiguous DNA sequences.

Sequence alignments and percent identity calculations can be performed using the Megalign program of the LASERGENE bioinformatics computing suite (DNASTAR Inc., Madison, Wis.). Multiple alignment of the sequences can be performed using the Clustal method of alignment (Higgins and Sharp (1989) *CABIOS*. 5:151-153) with the default parameters (GAP PENALTY=10, GAP LENGTH PENALTY=10). Default parameters for pairwise alignments using the Clustal method are KTUPLE 1, GAP PENALTY=3, WINDOW=5 and DIAGONALS SAVED=5.

EXAMPLE 5

This example describes expression of transgenes in monocot cells.

A transgene can be constructed comprising a cDNA encoding the instant polypeptides, such as ipt (SEQ ID NO: 2) or ivr2 (SEQ ID NO: 20), in sense orientation with respect to a maize silk-preferred promoter, such as gl2 (SEQ ID NO: 1 or 26), that is located 5' to the cDNA fragment, and an appropriate termination sequence, such as the 10 kD zein 3' end, located 3' to the cDNA fragment. The cDNA fragment of this gene may be generated by polymerase chain reaction (PCR) of the cDNA clone using appropriate oligonucleotide primers. Cloning sites (NcoI or SmaI) can be incorporated into the oligonucleotides to provide proper orientation of the DNA fragment when inserted into the digested vector pML103 as described below. Amplification is then performed in a standard PCR. The amplified DNA is then digested with restriction enzymes NcoI and SmaI and fractionated on an agarose gel. The appropriate band can be isolated from the gel and combined with a 4.9 kb NcoI-SmaI fragment of the plasmid pML103. Plasmid pML103 has been deposited under the terms of the Budapest Treaty at ATCC (American Type Culture Collection, 10801 University Blvd., Manassas, Va. 20110-2209), and bears accession number ATCC 97366. The DNA segment from pML103 contains a 1.05 kb SalI-NcoI promoter fragment of the maize 27 kD zein gene and a 0.96 kb SmaI-SalI fragment from the 3' end of the maize 10 kD zein gene in the vector pGem9Zf(+) (Promega). Vector and insert DNA can be ligated at 15° C. overnight, essentially as described (Maniatis). The ligated DNA may then be used to transform *E. coli* XL1-Blue (*Epicurian Coli* XL-1 Blue; Stratagene). Bacterial transformants can be screened by restriction enzyme digestion of plasmid DNA and limited nucleotide sequence analysis using the dideoxy chain termination method (Sequenase DNA Sequencing Kit; U. S. Biochemical). The resulting plasmid construct would comprise a transgene encoding, in the 5' to 3' direction, the maize 27 kD zein promoter, a cDNA fragment encoding the instant polypeptides, and the 10 kD zein 3' region.

The transgene described above can then be introduced into corn cells by the following procedure. Immature corn

embryos can be dissected from developing caryopses derived from crosses of the inbred corn lines H99 and LH132. The embryos are isolated 10 to 11 days after pollination when they are 1.0 to 1.5 mm long. The embryos are then placed with the axis-side facing down and in contact with agarose-solidified N6 medium (Chu et al. (1975) *Sci. Sin. Peking* 18:659-668). The embryos are kept in the dark at 27° C. Friable embryogenic callus consisting of undifferentiated masses of cells with somatic proembryoids and embryoids borne on suspensor structures proliferates from the scutellum of these immature embryos. The embryogenic callus isolated from the primary explant can be cultured on N6 medium and sub-cultured on this medium every 2 to 3 weeks.

The plasmid, p35S/Ac (Hoechst Ag, Frankfurt, Germany) or equivalent may be used in transformation experiments in order to provide for a selectable marker. This plasmid contains the Pat gene (see European Patent Publication 0 242 236) which encodes phosphinothricin acetyl transferase (PAT). The enzyme PAT confers resistance to herbicidal glutamine synthetase inhibitors such as phosphinothricin. The pat gene in p35S/Ac is under the control of the 35S promoter from Cauliflower Mosaic Virus (Odell et al., (1985) *Nature* 313:810-812) and the 3' region of the nopaline synthase gene from the T-DNA of the Ti plasmid of *Agrobacterium tumefaciens*.

The particle bombardment method (Klein et al., (1987) *Nature* 327:70-73) may be used to transfer genes to the callus culture cells. According to this method, gold particles (1 µm in diameter) are coated with DNA using the following technique. Ten µg of plasmid DNAs are added to 50 µL of a suspension of gold particles (60 mg per mL). Calcium chloride (50 µL of a 2.5 M solution) and spermidine free base (20 µL of a 1.0 M solution) are added to the particles. The suspension is vortexed during the addition of these solutions. After 10 minutes, the tubes are briefly centrifuged (5 sec at 15,000 rpm) and the supernatant removed. The particles are resuspended in 200 µL of absolute ethanol, centrifuged again and the supernatant removed. The ethanol rinse is performed again and the particles resuspended in a final volume of 30 µL of ethanol. An aliquot (5 µL) of the DNA-coated gold particles can be placed in the center of a Kapton flying disc (Bio-Rad Labs). The particles are then accelerated into the corn tissue with a Biolistic PDS-1000/He (Bio-Rad Instruments, Hercules Calif.), using a helium pressure of 1000 psi, a gap distance of 0.5 cm and a flying distance of 1.0 cm.

For bombardment, the embryogenic tissue is placed on filter paper over agarose-solidified N6 medium. The tissue is arranged as a thin lawn and covered a circular area of about 5 cm in diameter. The petri dish containing the tissue can be placed in the chamber of the PDS-1000/He approximately 8 cm from the stopping screen. The air in the chamber is then evacuated to a vacuum of 28 inches of Hg. The macrocarrier is accelerated with a helium shock wave using a rupture membrane that bursts when the He pressure in the shock tube reaches 1000 psi.

Seven days after bombardment the tissue can be transferred to N6 medium that contains glufosinate (2 mg per liter) and lacks casein or proline. The tissue continues to grow slowly on this medium. After an additional 2 weeks the tissue can be transferred to fresh N6 medium containing glufosinate. After 6 weeks, areas of about 1 cm in diameter of actively growing callus can be identified on some of the plates containing the glufosinate-supplemented medium. These calli may continue to grow when sub-cultured on the selective medium.

Plants can be regenerated from the transgenic callus by first transferring clusters of tissue to N6 medium supplemented with 0.2 mg per liter of 2,4-D. After two weeks the tissue can be transferred to regeneration medium (Fromm et al., (1990) *Bio/Technology* 8:833-839).

EXAMPLE 6

This example describes expression of transgenes in dicot cells.

A seed-specific expression cassette composed of the promoter and transcription terminator from the gene encoding the β subunit of the seed storage protein phaseolin from the bean *Phaseolus vulgaris* (Doyle et al., (1986) *J. Biol. Chem.* 261:9228-9238) can be used for expression of the instant polypeptides in transformed soybean. The phaseolin cassette includes about 500 nucleotides upstream (5') from the translation initiation codon and about 1650 nucleotides downstream (3') from the translation stop codon of phaseolin. Between the 5' and 3' regions are the unique restriction endonuclease sites Nco I (which includes the ATG translation initiation codon), SmaI, KpnI and XbaI. The entire cassette is flanked by Hind III sites.

The cDNA fragment of this gene may be generated by polymerase chain reaction (PCR) of the cDNA clone using appropriate oligonucleotide primers. Cloning sites can be incorporated into the oligonucleotides to provide proper orientation of the DNA fragment when inserted into the expression vector. Amplification is then performed as described above, and the isolated fragment is inserted into a pUC18 vector carrying the seed expression cassette.

Soybean embryos may then be transformed with the expression vector comprising sequences encoding the instant polypeptides. To induce somatic embryos, cotyledons, 3-5 mm in length dissected from surface sterilized, immature seeds of the soybean cultivar A2872, can be cultured in the light or dark at 26° C. on an appropriate agar medium for 6-10 weeks. Somatic embryos which produce secondary embryos are then excised and placed into a suitable liquid medium. After repeated selection for clusters of somatic embryos which multiplied as early, globular staged embryos, the suspensions are maintained as described below.

Soybean embryogenic suspension cultures can be maintained in 35 mL liquid media on a rotary shaker, 150 rpm, at 26° C. with florescent lights on a 16:8 hour day/night schedule. Cultures are subcultured every two weeks by inoculating approximately 35 mg of tissue into 35 mL of liquid medium.

Soybean embryogenic suspension cultures may then be transformed by the method of particle gun bombardment (Klein et al., (1987) *Nature* (London) 327:70-73, U.S. Pat. No. 4,945,050). A Du Pont Biolistic PDS1000/HE instrument (helium retrofit) can be used for these transformations.

A selectable marker gene which can be used to facilitate soybean transformation is a transgene composed of the 35S promoter from Cauliflower Mosaic Virus (Odell et al., (1985) *Nature* 313:810-812), the hygromycin phosphotransferase gene from plasmid pJR225 (from *E. coli*; Gritz et al., (1983) *Gene* 25:179-188) and the 3' region of the nopaline synthase gene from the T-DNA of the Ti plasmid of *Agrobacterium tumefaciens*. The seed expression cassette comprising the phaseolin 5' region, the fragment encoding the instant polypeptide and the phaseolin 3' region can be isolated as a restriction fragment. This fragment can then be inserted into a unique restriction site of the vector carrying the marker gene.

To 50 μ L of a 60 mg/mL 1 μ m gold particle suspension are added (in order): 5 μ L DNA (1 μ g/ μ L), 20 μ L spermidine (0.1 M), and 50 μ L CaCl_2 (2.5 M). The particle preparation is then agitated for three minutes, spun in a microfuge for 10 seconds and the supernatant removed. The DNA-coated particles are then washed once in 400 μ L 70% ethanol and resuspended in 40 μ L of anhydrous ethanol. The DNA/particle suspension can be sonicated three times for one second each. Five microliters of the DNA-coated gold particles are then loaded on each macro carrier disk.

Approximately 300-400 mg of a two-week-old suspension culture is placed in an empty 60 \times 15 mm petri dish and the residual liquid removed from the tissue with a pipette. For each transformation experiment, approximately 5-10 plates of tissue are normally bombarded. Membrane rupture pressure is set at 1100 psi and the chamber is evacuated to a vacuum of 28 inches mercury. The tissue is placed approximately 3.5 inches away from the retaining screen and bombarded three times. Following bombardment, the tissue can be divided in half and placed back into liquid and cultured as described above.

Five to seven days post bombardment, the liquid media may be exchanged with fresh media, and eleven to twelve days post bombardment with fresh media containing 50 mg/mL hygromycin. This selective media can be refreshed weekly. Seven to eight weeks post bombardment, green, transformed tissue may be observed growing from untransformed, necrotic embryogenic clusters. Isolated green tissue is removed and inoculated into individual flasks to generate new, clonally propagated, transformed embryogenic suspension cultures. Each new line may be treated as an independent transformation event. These suspensions can then be subcultured and maintained as clusters of immature embryos or regenerated into whole plants by maturation and germination of individual somatic embryos.

EXAMPLE 7

This example describes expression of a transgene in microbial cells.

The cDNAs encoding the instant polypeptides can be inserted into the T7 *E. coli* expression vector pBT430. This vector is a derivative of pET-3a (Rosenberg et al., (1987) *Gene* 56:125-135) which employs the bacteriophage T7 RNA polymerase/T7 promoter system. Plasmid pBT430 was constructed by first destroying the EcoR I and Hind III sites in pET-3a at their original positions. An oligonucleotide adaptor containing EcoR I and Hind III sites was inserted at the BamH I site of pET-3a. This created pET-3aM with additional unique cloning sites for insertion of genes into the expression vector. Then, the Nde I site at the position of translation initiation was converted to an Nco I site using oligonucleotide-directed mutagenesis. The DNA sequence of pET-3aM in this region, 5'-CATATGG, was converted to 5'-CCCATGG in pBT430.

Plasmid DNA containing a cDNA may be appropriately digested to release a nucleic acid fragment encoding the protein. This fragment may then be purified on a 1% NuSieve GTG low melting agarose gel (FMC). Buffer and agarose contain 10 μ g/ml ethidium bromide for visualization of the DNA fragment. The fragment can then be purified from the agarose gel by digestion with GELase (Epicentre Technologies) according to the manufacturer's instructions, ethanol precipitated, dried and resuspended in 20 μ L of water. Appropriate oligonucleotide adapters may be ligated to the fragment using T4 DNA ligase (New England Biolabs, Beverly, Mass.). The fragment containing the ligated adapters can be purified from the excess adapters using low melting agarose as described above. The vector pBT430 is digested, dephosphorylated with alkaline phosphatase (NEB) and deproteinized with phenol/chloroform as described above. The prepared vector pBT430 and fragment can then be ligated at 16 $^\circ$ C. for 15 hours followed by transformation into DH5 electrocompetent cells (GIBCO BRL). Transformants can be selected on agar plates containing LB media and 100 μ g/mL ampicillin. Transformants containing the gene encoding the instant polypeptides are then screened for the correct orientation with respect to the T7 promoter by restriction enzyme analysis.

For high level expression, a plasmid clone with the cDNA insert in the correct orientation relative to the T7 promoter can be transformed into *E. coli* strain BL21 (DE3) (Studier et al., (1986) *J. Mol. Biol.* 189:113-130). Cultures are grown in LB medium containing ampicillin (100 mg/L) at 25 $^\circ$ C. At an optical density at 600 nm of approximately 1, IPTG (isopropylthio- β -galactoside, the inducer) can be added to a final concentration of 0.4 mM and incubation can be continued for 3 h at 25 $^\circ$. Cells are then harvested by centrifugation and re-suspended in 50 μ L of 50 mM Tris-HCl at pH 8.0 containing 0.1 mM DTT and 0.2 mM phenyl methylsulfonyl fluoride. A small amount of 1 mm glass beads can be added and the mixture sonicated 3 times for about 5 seconds each time with a microprobe sonicator. The mixture is centrifuged and the protein concentration of the supernatant determined. One microgram of protein from the soluble fraction of the culture can be separated by SDS-polyacrylamide gel electrophoresis. Gels can be observed for protein bands migrating at the expected molecular weight.

The above examples are provided to illustrate the invention but not to limit its scope. Other variants of the invention will be readily apparent to one of ordinary skill in the art and are encompassed by the appended claims. All publications, patents, patent applications, and computer programs cited herein are hereby incorporated by reference.

SEQUENCE LISTING

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cccgccacag gccacatcgt ttccggcctt gctcggctat atatccgca gcactctgat   1860
atcgccatat ccccgccccg ggcaccgcca gctagctagc tactgacacc cggcgccggc   1920
gccgagtaca atacaaggaa agcacc                                     1946

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<210> SEQ ID NO 2

<211> LENGTH: 723

<212> TYPE: DNA

<213> ORGANISM: Zea mays

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1)...(720)

<400> SEQUENCE: 2

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atg gat cta cgt cta att ttc ggt cca act tgc aca gga aag aca tcg	48
Met Asp Leu Arg Leu Ile Phe Gly Pro Thr Cys Thr Gly Lys Thr Ser	
1 5 10 15	
act gcg ata gct ctt gcc cag cag act ggc ctc cca gtc ctc tcg ctc	96
Thr Ala Ile Ala Leu Ala Gln Gln Thr Gly Leu Pro Val Leu Ser Leu	
20 25 30	
gat cgc gtc caa tgc tgt cct caa cta tca acc gga agc ggg cga cca	144
Asp Arg Val Gln Cys Cys Pro Gln Leu Ser Thr Gly Ser Gly Arg Pro	
35 40 45	
aca gtg gaa gaa ctg aaa gga acg act cgt ctg tac ctt gat gat cgc	192
Thr Val Glu Glu Leu Lys Gly Thr Thr Arg Leu Tyr Leu Asp Asp Arg	
50 55 60	
cct ttg gta aag ggt atc att aca gcc aag caa gct cat gaa cgg ctc	240
Pro Leu Val Lys Gly Ile Ile Thr Ala Lys Gln Ala His Glu Arg Leu	
65 70 75 80	
att gcg gag gtg cac aat cac gag gcc aaa ggc ggg ctt att ctt gag	288
Ile Ala Glu Val His Asn His Glu Ala Lys Gly Gly Leu Ile Leu Glu	
85 90 95	
gga gga tct atc tcg ttg ctc agg tgc atg gcg caa agt cgt tat tgg	336
Gly Gly Ser Ile Ser Leu Leu Arg Cys Met Ala Gln Ser Arg Tyr Trp	
100 105 110	
aac gcg gat ttt cgt tgg cat att att cgc aac gag tta gca gac gag	384
Asn Ala Asp Phe Arg Trp His Ile Ile Arg Asn Glu Leu Ala Asp Glu	
115 120 125	
gag agc ttc atg agc gtg gcc aag acc aga gtt aag cag atg tta cgc	432
Glu Ser Phe Met Ser Val Ala Lys Thr Arg Val Lys Gln Met Leu Arg	
130 135 140	
ccc tct gca ggt ctt tct att atc caa gag ttg gtt caa ctt tgg agg	480
Pro Ser Ala Gly Leu Ser Ile Ile Gln Glu Leu Val Gln Leu Trp Arg	
145 150 155 160	
gag cct cgg ctg agg ccc ata ctg gaa ggg atc gat gga tat cga tat	528
Glu Pro Arg Leu Arg Pro Ile Leu Glu Gly Ile Asp Gly Tyr Arg Tyr	
165 170 175	
gcc ctg cta ttt gct acc cag aac cag atc acg ccc gat atg cta ttg	576
Ala Leu Leu Phe Ala Thr Gln Asn Gln Ile Thr Pro Asp Met Leu Leu	
180 185 190	
cag ctc gac gca gat atg gag aat aaa ttg att cac ggt atc gct cag	624
Gln Leu Asp Ala Asp Met Glu Asn Lys Leu Ile His Gly Ile Ala Gln	
195 200 205	
gag ttt cta atc cat gcg cgt cga cag gaa cag aaa ttc cct ttg gtg	672
Glu Phe Leu Ile His Ala Arg Arg Gln Glu Gln Lys Phe Pro Leu Val	
210 215 220	
ggc gcg aca gct gtc gaa gcg ttt gaa gga cca cca ttt cga atg tga	720
Gly Ala Thr Ala Val Glu Ala Phe Glu Gly Pro Pro Phe Arg Met *	
225 230 235	
ggt	723

<210> SEQ ID NO 3
 <211> LENGTH: 239
 <212> TYPE: PRT
 <213> ORGANISM: Zea mays

<400> SEQUENCE: 3

Met Asp Leu Arg Leu Ile Phe Gly Pro Thr Cys Thr Gly Lys Thr Ser
1 5 10 15
Thr Ala Ile Ala Leu Ala Gln Gln Thr Gly Leu Pro Val Leu Ser Leu
20 25 30
Asp Arg Val Gln Cys Cys Pro Gln Leu Ser Thr Gly Ser Gly Arg Pro
35 40 45

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Thr	Val	Glu	Glu	Leu	Lys	Gly	Thr	Thr	Arg	Leu	Tyr	Leu	Asp	Asp	Arg
	50					55					60				
Pro	Leu	Val	Lys	Gly	Ile	Ile	Thr	Ala	Lys	Gln	Ala	His	Glu	Arg	Leu
	65				70					75					80
Ile	Ala	Glu	Val	His	Asn	His	Glu	Ala	Lys	Gly	Gly	Leu	Ile	Leu	Glu
				85					90					95	
Gly	Gly	Ser	Ile	Ser	Leu	Leu	Arg	Cys	Met	Ala	Gln	Ser	Arg	Tyr	Trp
			100					105					110		
Asn	Ala	Asp	Phe	Arg	Trp	His	Ile	Ile	Arg	Asn	Glu	Leu	Ala	Asp	Glu
		115					120					125			
Glu	Ser	Phe	Met	Ser	Val	Ala	Lys	Thr	Arg	Val	Lys	Gln	Met	Leu	Arg
	130					135					140				
Pro	Ser	Ala	Gly	Leu	Ser	Ile	Ile	Gln	Glu	Leu	Val	Gln	Leu	Trp	Arg
	145				150					155					160
Glu	Pro	Arg	Leu	Arg	Pro	Ile	Leu	Glu	Gly	Ile	Asp	Gly	Tyr	Arg	Tyr
			165						170					175	
Ala	Leu	Leu	Phe	Ala	Thr	Gln	Asn	Gln	Ile	Thr	Pro	Asp	Met	Leu	Leu
			180					185					190		
Gln	Leu	Asp	Ala	Asp	Met	Glu	Asn	Lys	Leu	Ile	His	Gly	Ile	Ala	Gln
		195					200					205			
Glu	Phe	Leu	Ile	His	Ala	Arg	Arg	Gln	Glu	Gln	Lys	Phe	Pro	Leu	Val
	210					215					220				
Gly	Ala	Thr	Ala	Val	Glu	Ala	Phe	Glu	Gly	Pro	Pro	Phe	Arg	Met	
	225				230					235					

<210> SEQ ID NO 4
 <211> LENGTH: 1077
 <212> TYPE: DNA
 <213> ORGANISM: Zea mays
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)...(1077)

<400> SEQUENCE: 4

atg	gtg	ccg	ggc	tat	gac	tgc	gcc	gcc	tcc	gtg	ctg	ctg	tgc	gcg	gag	48
Met	Val	Pro	Gly	Tyr	Asp	Cys	Ala	Ala	Ser	Val	Leu	Leu	Cys	Ala	Glu	
1			5						10					15		
ac	aac	gct	gct	att	ctc	ggc	ctg	gac	gac	gat	ggg	gag	gag	tcc	tcc	96
Asp	Asn	Ala	Ala	Ile	Leu	Gly	Leu	Asp	Asp	Asp	Gly	Glu	Glu	Ser	Ser	
			20					25					30			
tgg	gcg	gcc	gcc	gct	acg	ccg	cca	cgt	gac	acc	gtc	gcc	gcc	gcc	gcc	144
Trp	Ala	Ala	Ala	Ala	Thr	Pro	Pro	Arg	Asp	Thr	Val	Ala	Ala	Ala	Ala	
			35					40				45				
gcc	acc	ggg	gtc	gcc	gtc	gat	ggg	att	ttg	acg	gag	ttc	ccc	ttg	ctc	192
Ala	Thr	Gly	Val	Ala	Val	Asp	Gly	Ile	Leu	Thr	Glu	Phe	Pro	Leu	Leu	
	50					55					60					
tcg	gat	gac	tgc	ggt	gcg	acg	ctc	gtg	gag	aag	gag	gtg	gag	cac	atg	240
Ser	Asp	Asp	Cys	Val	Ala	Thr	Leu	Val	Glu	Lys	Glu	Val	Glu	His	Met	
	65				70					75					80	
ccc	gcg	gag	ggg	tac	ctc	cag	aag	ctg	cag	cga	cgg	cat	ggg	gac	ctg	288
Pro	Ala	Glu	Gly	Tyr	Leu	Gln	Lys	Leu	Gln	Arg	Arg	His	Gly	Asp	Leu	
				85					90					95		
gat	ttg	gcc	gcc	gtc	agg	aag	gac	gcc	atc	gat	tgg	att	tgg	aag	gtc	336
Asp	Leu	Ala	Ala	Val	Arg	Lys	Asp	Ala	Ile	Asp	Trp	Ile	Trp	Lys	Val	
			100					105					110			
att	gag	cat	tac	aat	ttc	gca	ccg	ttg	act	gcc	ggt	ttg	tct	gtg	aac	384
Ile	Glu	His	Tyr	Asn	Phe	Ala	Pro	Leu	Thr	Ala	Val	Leu	Ser	Val	Asn	
		115					120						125			

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tac ctc gat aga ttc ctc tcc acg tat gag ttc cct gaa ggc aga gct	432
Tyr Leu Asp Arg Phe Leu Ser Thr Tyr Glu Phe Pro Glu Gly Arg Ala	
130 135 140	
tgg atg act cag ctc ttg gca gtg gct tgc ttg tct ttg gct tcg aaa	480
Trp Met Thr Gln Leu Leu Ala Val Ala Cys Leu Ser Leu Ala Ser Lys	
145 150 155 160	
atc gaa gag act ttt gtg cca ctc ccc ttg gat ttg cag gta gcg gag	528
Ile Glu Glu Thr Phe Val Pro Leu Pro Leu Asp Leu Gln Val Ala Glu	
165 170 175	
gca aag ttt gtt ttt gag gga agg acc ata aaa agg atg gag ctt ctg	576
Ala Lys Phe Val Phe Glu Gly Arg Thr Ile Lys Arg Met Glu Leu Leu	
180 185 190	
gtg cta agc acc tta aag tgg agg atg cat gct gtt act gct tgc tca	624
Val Leu Ser Thr Leu Lys Trp Arg Met His Ala Val Thr Ala Cys Ser	
195 200 205	
ttt gtt gaa tac ttt ctt cat aaa ttg agt gat cat ggt gca ccc tcc	672
Phe Val Glu Tyr Phe Leu His Lys Leu Ser Asp His Gly Ala Pro Ser	
210 215 220	
ttg ctt gca cgc tct cgc tct ttg gac ctt gtc ttg agc acc gct aaa	720
Leu Leu Ala Arg Ser Arg Ser Leu Asp Leu Val Leu Ser Thr Ala Lys	
225 230 235 240	
ggt gct gaa ttc gtg gta ttc aga ccc tcc gag att gct gcc agt gtt	768
Gly Ala Glu Phe Val Val Phe Arg Pro Ser Glu Ile Ala Ala Ser Val	
245 250 255	
gca ctt gct gct atc ggc gaa tgc agg agt tct gta att gag aga gct	816
Ala Leu Ala Ala Ile Glu Gly Glu Cys Arg Ser Ser Val Ile Glu Arg Ala	
260 265 270	
gct agt agc tgc aaa tat ttg gac aag gag agg gtt tta aga tgc cat	864
Ala Ser Ser Cys Lys Tyr Leu Asp Lys Glu Arg Val Leu Arg Cys His	
275 280 285	
gaa atg att caa gag aag att act gcg gga agc att gtc cta aag tct	912
Glu Met Ile Gln Glu Lys Ile Thr Ala Gly Ser Ile Val Leu Lys Ser	
290 295 300	
gct gga tca tca atc tcc tct gtg cca caa agc cca ata ggt gtc ctg	960
Ala Gly Ser Ser Ile Ser Ser Val Pro Gln Ser Pro Ile Gly Val Leu	
305 310 315 320	
gac gct gca gcc tgt ctg agt caa caa agc gat gac gct act gtc ggg	1008
Asp Ala Ala Ala Cys Leu Ser Gln Gln Ser Asp Asp Ala Thr Val Gly	
325 330 335	
tct cct gca gta tgt tac cat agt tct tcc aca agc aag agg aga agg	1056
Ser Pro Ala Val Cys Tyr His Ser Ser Ser Thr Ser Lys Arg Arg Arg	
340 345 350	
atc act aga cgt cta ctc taa	1077
Ile Thr Arg Arg Leu Leu *	
355	

<210> SEQ ID NO 5
 <211> LENGTH: 358
 <212> TYPE: PRT
 <213> ORGANISM: Zea mays

<400> SEQUENCE: 5

Met Val Pro Gly Tyr Asp Cys Ala Ala Ser Val Leu Leu Cys Ala Glu
1 5 10 15
Asp Asn Ala Ala Ile Leu Gly Leu Asp Asp Asp Gly Glu Glu Ser Ser
20 25 30
Trp Ala Ala Ala Ala Thr Pro Pro Arg Asp Thr Val Ala Ala Ala Ala
35 40 45
Ala Thr Gly Val Ala Val Asp Gly Ile Leu Thr Glu Phe Pro Leu Leu
50 55 60

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Ser Asp Asp Cys Val Ala Thr Leu Val Glu Lys Glu Val Glu His Met
 65 70 75 80

Pro Ala Glu Gly Tyr Leu Gln Lys Leu Gln Arg Arg His Gly Asp Leu
 85 90 95

Asp Leu Ala Ala Val Arg Lys Asp Ala Ile Asp Trp Ile Trp Lys Val
 100 105 110

Ile Glu His Tyr Asn Phe Ala Pro Leu Thr Ala Val Leu Ser Val Asn
 115 120 125

Tyr Leu Asp Arg Phe Leu Ser Thr Tyr Glu Phe Pro Glu Gly Arg Ala
 130 135 140

Trp Met Thr Gln Leu Leu Ala Val Ala Cys Leu Ser Leu Ala Ser Lys
 145 150 155 160

Ile Glu Glu Thr Phe Val Pro Leu Pro Leu Asp Leu Gln Val Ala Glu
 165 170 175

Ala Lys Phe Val Phe Glu Gly Arg Thr Ile Lys Arg Met Glu Leu Leu
 180 185 190

Val Leu Ser Thr Leu Lys Trp Arg Met His Ala Val Thr Ala Cys Ser
 195 200 205

Phe Val Glu Tyr Phe Leu His Lys Leu Ser Asp His Gly Ala Pro Ser
 210 215 220

Leu Leu Ala Arg Ser Arg Ser Leu Asp Leu Val Leu Ser Thr Ala Lys
 225 230 235 240

Gly Ala Glu Phe Val Val Phe Arg Pro Ser Glu Ile Ala Ala Ser Val
 245 250 255

Ala Leu Ala Ala Ile Gly Glu Cys Arg Ser Ser Val Ile Glu Arg Ala
 260 265 270

Ala Ser Ser Cys Lys Tyr Leu Asp Lys Glu Arg Val Leu Arg Cys His
 275 280 285

Glu Met Ile Gln Glu Lys Ile Thr Ala Gly Ser Ile Val Leu Lys Ser
 290 295 300

Ala Gly Ser Ser Ile Ser Ser Val Pro Gln Ser Pro Ile Gly Val Leu
 305 310 315 320

Asp Ala Ala Ala Cys Leu Ser Gln Gln Ser Asp Asp Ala Thr Val Gly
 325 330 335

Ser Pro Ala Val Cys Tyr His Ser Ser Ser Thr Ser Lys Arg Arg Arg
 340 345 350

Ile Thr Arg Arg Leu Leu
 355

<210> SEQ ID NO 6
 <211> LENGTH: 876
 <212> TYPE: DNA
 <213> ORGANISM: Zea mays
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)...(876)

<400> SEQUENCE: 6

atg gac cag tac gag aag gtg gag aag atc ggg gag ggc acg tac ggg 48
 Met Asp Gln Tyr Glu Lys Val Glu Lys Ile Gly Glu Gly Thr Tyr Gly
 1 5 10 15

gtg gtg tac aag ggc aag gac cgc cac acc aac gag acg atc gcg ctc 96
 Val Val Tyr Lys Gly Lys Asp Arg His Thr Asn Glu Thr Ile Ala Leu
 20 25 30

aag aag atc cgc ctc gag cag gag gac gag ggc gtc ccc tcc acc gcc 144
 Lys Lys Ile Arg Leu Glu Gln Glu Asp Glu Gly Val Pro Ser Thr Ala

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35			40			45										
atc	cgc	gag	atc	tcc	ctc	ctc	aag	gag	atg	cag	cac	cgc	aac	atc	gtc	192
Ile	Arg	Glu	Ile	Ser	Leu	Leu	Lys	Glu	Met	Gln	His	Arg	Asn	Ile	Val	
	50				55					60						
agg	ctg	cag	gaa	gtc	gtg	cac	aac	gac	aag	tgc	atc	tac	ctc	gtc	ttc	240
Arg	Leu	Gln	Glu	Val	Val	His	Asn	Asp	Lys	Cys	Ile	Tyr	Leu	Val	Phe	
	65			70						75				80		
gag	tac	ctc	gac	ctc	gac	ctc	aag	aag	cac	atg	gac	tcc	tcc	acg	gac	288
Glu	Tyr	Leu	Asp	Leu	Asp	Leu	Lys	Lys	His	Met	Asp	Ser	Ser	Thr	Asp	
			85						90					95		
ttc	aag	aac	cac	cgc	ata	gtc	aaa	tcc	ttc	ctc	tac	cag	att	ctg	cgg	336
Phe	Lys	Asn	His	Arg	Ile	Val	Lys	Ser	Phe	Leu	Tyr	Gln	Ile	Leu	Arg	
			100					105					110			
ggc	atc	gcc	tac	tgc	cac	tcg	cac	cgc	gtg	ctc	cac	cgc	gac	ctg	aag	384
Gly	Ile	Ala	Tyr	Cys	His	Ser	His	Arg	Val	Leu	His	Arg	Asp	Leu	Lys	
		115						120					125			
ccg	cag	aac	ctg	ctg	att	gac	cgc	cgc	aac	aac	ctc	ttg	aag	ctc	gcg	432
Pro	Gln	Asn	Leu	Leu	Ile	Asp	Arg	Arg	Asn	Asn	Leu	Leu	Lys	Leu	Ala	
		130						135						140		
gac	ttt	gga	ctg	gcg	agg	gcg	ttc	ggc	atc	cct	gtc	cgg	acg	ttc	act	480
Asp	Phe	Gly	Leu	Ala	Arg	Ala	Phe	Gly	Ile	Pro	Val	Arg	Thr	Phe	Thr	
				150						155				160		
cat	gag	gtg	gtg	acg	ctt	tgg	tat	aga	gcg	cct	gaa	atc	ctt	ctc	ggt	528
His	Glu	Val	Val	Thr	Leu	Trp	Tyr	Arg	Ala	Pro	Glu	Ile	Leu	Leu	Gly	
				165						170				175		
gca	agg	cat	tat	tcc	acc	cct	ggt	gat	gtg	tgg	tca	ggt	ggt	tgc	att	576
Ala	Arg	His	Tyr	Ser	Thr	Pro	Val	Asp	Val	Trp	Ser	Val	Gly	Cys	Ile	
			180					185					190			
ttc	gct	gaa	atg	gtg	aac	cag	aag	gcg	ctt	ttt	cct	ggc	gac	tct	gag	624
Phe	Ala	Glu	Met	Val	Asn	Gln	Lys	Ala	Leu	Phe	Pro	Gly	Asp	Ser	Glu	
		195						200					205			
atc	gat	gag	ctg	ttt	aag	att	ttc	aga	att	ttg	ggc	act	cca	act	aaa	672
Ile	Asp	Glu	Leu	Phe	Lys	Ile	Phe	Arg	Ile	Leu	Gly	Thr	Pro	Thr	Lys	
		210						215						220		
gaa	aca	tgg	cca	ggc	ggt	gct	tcg	ttg	cct	gat	tac	aag	tca	act	ttc	720
Glu	Thr	Trp	Pro	Gly	Val	Ala	Ser	Leu	Pro	Asp	Tyr	Lys	Ser	Thr	Phe	
		225			230					235				240		
cca	aag	tgg	cca	cct	gtg	gat	ctt	gca	acg	gtg	gtc	ccg	aca	ctc	gaa	768
Pro	Lys	Trp	Pro	Pro	Val	Asp	Leu	Ala	Thr	Val	Val	Pro	Thr	Leu	Glu	
				245						250				255		
ccg	tcg	gga	atc	gat	ctc	cta	tct	aag	atg	ctg	cgt	cta	gat	ccc	agc	816
Pro	Ser	Gly	Ile	Asp	Leu	Leu	Ser	Lys	Met	Leu	Arg	Leu	Asp	Pro	Ser	
			260					265					270			
aag	agg	atc	acc	gcc	cgc	gcc	gcc	ctc	gag	cac	gac	tac	ttc	agg	gac	864
Lys	Arg	Ile	Thr	Ala	Arg	Ala	Ala	Leu	Glu	His	Asp	Tyr	Phe	Arg	Asp	
		275						280					285			
ctc	gag	cac	gcc													876
Leu	Glu	His	Ala													
		290														
<210> SEQ ID NO 7																
<211> LENGTH: 292																
<212> TYPE: PRT																
<213> ORGANISM: Zea mays																
<400> SEQUENCE: 7																
Met	Asp	Gln	Tyr	Glu	Lys	Val	Glu	Lys	Ile	Gly	Glu	Gly	Thr	Tyr	Gly	
1				5					10					15		
Val	Val	Tyr	Lys	Gly	Lys	Asp	Arg	His	Thr	Asn	Glu	Thr	Ile	Ala	Leu	
			20					25					30			

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aac acg gcg gcg ctg agc acg gcg ctg ttc aac gac ggc gcc gcg tgc      240
Asn Thr Ala Ala Leu Ser Thr Ala Leu Phe Asn Asp Gly Ala Ala Cys
 65                70                75                80

ggg tcc tgc tac gag ctg cgc tgc gac aac aac ggg cag tcg tgc ctg      288
Gly Ser Cys Tyr Glu Leu Arg Cys Asp Asn Asn Gly Gln Ser Cys Leu
                85                90                95

ccg ggc acc atc acc gtc acg gcc acc aac ttc tgc ccg ccc aac tac      336
Pro Gly Thr Ile Thr Val Thr Ala Thr Asn Phe Cys Pro Pro Asn Tyr
                100                105                110

ggc ctc ccc agc gac gac ggc ggc tgg tgc aac ccg ccg cgc ccg cac      384
Gly Leu Pro Ser Asp Asp Gly Gly Trp Cys Asn Pro Pro Arg Pro His
                115                120                125

ttc gac atg gcc cag ccg gcc ttc ctc cag atc gcg cag tac cgc gcc      432
Phe Asp Met Ala Gln Pro Ala Phe Leu Gln Ile Ala Gln Tyr Arg Ala
 130                135                140

ggc atc gtg ccc gtc gcc tac agg agg gtg ccg tgc gtg aag aag ggc      480
Gly Ile Val Pro Val Ala Tyr Arg Arg Val Pro Cys Val Lys Lys Gly
 145                150                155                160

ggg atc agg ttc acc atc aac ggc cac tcc tac ttc aac ctg gtg ctg      528
Gly Ile Arg Phe Thr Ile Asn Gly His Ser Tyr Phe Asn Leu Val Leu
                165                170                175

gtg acc aac gtg gcc ggc gcc ggg gac gtg cag tcc gtg tcc atc aag      576
Val Thr Asn Val Ala Gly Ala Gly Asp Val Gln Ser Val Ser Ile Lys
                180                185                190

ggc tcc agc acc ggg tgg cag ccc atg tcc cgc aac tgg ggc cag aac      624
Gly Ser Ser Thr Gly Trp Gln Pro Met Ser Arg Asn Trp Gly Gln Asn
                195                200                205

tgg cag agc aac tcg ctc ctc gac ggc cag agc ctg tcc ttc cag gtc      672
Trp Gln Ser Asn Ser Leu Leu Asp Gly Gln Ser Leu Ser Phe Gln Val
 210                215                220

acc gcc agc gac ggc cgc acc gtc acc agc aac ggc gtc gct ccg gcg      720
Thr Ala Ser Asp Gly Arg Thr Val Thr Ser Asn Gly Val Ala Pro Ala
 225                230                235                240

ggc tgg cag ttc ggc cag acc ttc gag ggc gcc cag ttc      759
Gly Trp Gln Phe Gly Gln Thr Phe Glu Gly Ala Gln Phe
                245                250

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<210> SEQ ID NO 9
 <211> LENGTH: 253
 <212> TYPE: PRT
 <213> ORGANISM: Zea mays

<400> SEQUENCE: 9

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Met Ala Ala Ala Ala Ser Ala Leu Leu Leu Leu Leu Cys Ser Ala Phe
 1                5                10                15

Cys Ser Leu Ala His Arg Ala Ala Gly Val Asp Tyr Gly Ser Trp Gln
                20                25                30

Ser Ala His Ala Thr Phe Tyr Gly Gly Gly Asp Ala Ser Gly Thr Met
 35                40                45

Gly Gly Ala Cys Gly Tyr Gly Asn Met Tyr Ser Thr Gly Tyr Gly Thr
 50                55                60

Asn Thr Ala Ala Leu Ser Thr Ala Leu Phe Asn Asp Gly Ala Ala Cys
 65                70                75                80

Gly Ser Cys Tyr Glu Leu Arg Cys Asp Asn Asn Gly Gln Ser Cys Leu
 85                90                95

Pro Gly Thr Ile Thr Val Thr Ala Thr Asn Phe Cys Pro Pro Asn Tyr
 100                105                110

Gly Leu Pro Ser Asp Asp Gly Gly Trp Cys Asn Pro Pro Arg Pro His
 115                120                125

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Phe Asp Met Ala Gln Pro Ala Phe Leu Gln Ile Ala Gln Tyr Arg Ala
 130 135 140

Gly Ile Val Pro Val Ala Tyr Arg Arg Val Pro Cys Val Lys Lys Gly
 145 150 155 160

Gly Ile Arg Phe Thr Ile Asn Gly His Ser Tyr Phe Asn Leu Val Leu
 165 170 175

Val Thr Asn Val Ala Gly Ala Gly Asp Val Gln Ser Val Ser Ile Lys
 180 185 190

Gly Ser Ser Thr Gly Trp Gln Pro Met Ser Arg Asn Trp Gly Gln Asn
 195 200 205

Trp Gln Ser Asn Ser Leu Leu Asp Gly Gln Ser Leu Ser Phe Gln Val
 210 215 220

Thr Ala Ser Asp Gly Arg Thr Val Thr Ser Asn Gly Val Ala Pro Ala
 225 230 235 240

Gly Trp Gln Phe Gly Gln Thr Phe Glu Gly Ala Gln Phe
 245 250

<210> SEQ ID NO 10
 <211> LENGTH: 849
 <212> TYPE: DNA
 <213> ORGANISM: Zea mays
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)...(849)

<400> SEQUENCE: 10

atg ggc tcc cct tcc tcc ctc ccc gcc gcg gcg gcg ctc gtg ctc ctg 48
 Met Gly Ser Pro Ser Ser Leu Pro Ala Ala Ala Ala Leu Val Leu Leu
 1 5 10 15

gcc ctg ctc gcc gga gcc cag tgc cgc gag gcc cag ttc gac gcc gcg 96
 Ala Leu Leu Ala Gly Ala Gln Cys Arg Glu Ala Gln Phe Asp Ala Ala
 20 25 30

gac gcc ggc gcg gag aac ttc aac acc agc gag gcc gcc gtg tac tgg 144
 Asp Ala Gly Ala Glu Asn Phe Asn Thr Ser Glu Ala Ala Val Tyr Trp
 35 40 45

ggc ccc tgg cag aag gcc cgg gcc acc tgg tac gcc cag ccc aac ggc 192
 Gly Pro Trp Gln Lys Ala Arg Ala Thr Trp Tyr Gly Gln Pro Asn Gly
 50 55 60

gcc gcc ccg gac gac aac ggt ggt gcg tgc gcc ttc aag cac acc aac 240
 Ala Gly Pro Asp Asp Asn Gly Gly Ala Cys Gly Phe Lys His Thr Asn
 65 70 75 80

cag tac ccc ttc atg tcc atg ggc tcc tgc gga aac cag cca ttg ttc 288
 Gln Tyr Pro Phe Met Ser Met Gly Ser Cys Gly Asn Gln Pro Leu Phe
 85 90 95

aag gac ggc aag gga tgc gcc tcc tgc tac aag att cgg tgc agg aag 336
 Lys Asp Gly Lys Gly Cys Gly Ser Cys Tyr Lys Ile Arg Cys Arg Lys
 100 105 110

gac ccg tcc tgc tcc ggg cgg acg gag acg gtg atc atc acc gac atg 384
 Asp Pro Ser Cys Ser Gly Arg Thr Glu Thr Val Ile Ile Thr Asp Met
 115 120 125

aac tac tac ccg gtg tcc aag tac cac ttc gac ctc agc gcc acg gcg 432
 Asn Tyr Tyr Pro Val Ser Lys Tyr His Phe Asp Leu Ser Gly Thr Ala
 130 135 140

ttc gcc agg ctg gcc aag ccc gcc ctc aac gac aag ctc cgc cac tcg 480
 Phe Gly Arg Leu Ala Lys Pro Gly Leu Asn Asp Lys Leu Arg His Ser
 145 150 155 160

ggc atc atc gac atc gag ttc acc agg gtg ccg tgc gag ttc cct gcc 528
 Gly Ile Ile Asp Ile Glu Phe Thr Arg Val Pro Cys Glu Phe Pro Gly
 165 170 175

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ctc aag atc ggg ttc cac gtg gag gag tac tcg aag ccc cgt cta ctt      576
Leu Lys Ile Gly Phe His Val Glu Glu Tyr Ser Lys Pro Arg Leu Leu
      180                      185                      190

cgc ggg tgc tgg tgg agt acg agg acg gcg aac ggc gac gtg gtg cag      624
Arg Gly Cys Trp Trp Ser Thr Arg Thr Ala Asn Gly Asp Val Val Gln
      195                      200                      205

gtg gac ctg atg gag tcc aag acg gcg cgc ggg ccg ccg acg ggg cgg      672
Val Asp Leu Met Glu Ser Lys Thr Ala Arg Gly Pro Pro Thr Gly Arg
      210                      215                      220

tgg gcg ccg atg cgc gag tcc tgg gcc tcc atc tgg cgc atg gac acc      720
Trp Ala Pro Met Arg Glu Ser Trp Gly Ser Ile Trp Arg Met Asp Thr
      225                      230                      235                      240

aac cac cgc atg cag ccg ccc ttc tcc atc cgc atc cgc aac gag tcc      768
Asn His Arg Met Gln Pro Pro Phe Ser Ile Arg Ile Arg Asn Glu Ser
      245                      250                      255

ggc aag acg ctc gtc gcc agg aac gtc atc ccg gcc aac tgg agg ccc      816
Gly Lys Thr Leu Val Ala Arg Asn Val Ile Pro Ala Asn Trp Arg Pro
      260                      265                      270

aac acc ttc tac cgc tcc ttc gtc cag tac agc                          849
Asn Thr Phe Tyr Arg Ser Phe Val Gln Tyr Ser
      275                      280

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<210> SEQ ID NO 11
<211> LENGTH: 283
<212> TYPE: PRT
<213> ORGANISM: Zea mays

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<400> SEQUENCE: 11

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Met Gly Ser Pro Ser Ser Leu Pro Ala Ala Ala Ala Leu Val Leu Leu
  1          5          10          15

Ala Leu Leu Ala Gly Ala Gln Cys Arg Glu Ala Gln Phe Asp Ala Ala
  20          25          30

Asp Ala Gly Ala Glu Asn Phe Asn Thr Ser Glu Ala Ala Val Tyr Trp
  35          40          45

Gly Pro Trp Gln Lys Ala Arg Ala Thr Trp Tyr Gly Gln Pro Asn Gly
  50          55          60

Ala Gly Pro Asp Asp Asn Gly Gly Ala Cys Gly Phe Lys His Thr Asn
  65          70          75          80

Gln Tyr Pro Phe Met Ser Met Gly Ser Cys Gly Asn Gln Pro Leu Phe
  85          90          95

Lys Asp Gly Lys Gly Cys Gly Ser Cys Tyr Lys Ile Arg Cys Arg Lys
  100         105         110

Asp Pro Ser Cys Ser Gly Arg Thr Glu Thr Val Ile Ile Thr Asp Met
  115         120         125

Asn Tyr Tyr Pro Val Ser Lys Tyr His Phe Asp Leu Ser Gly Thr Ala
  130         135         140

Phe Gly Arg Leu Ala Lys Pro Gly Leu Asn Asp Lys Leu Arg His Ser
  145         150         155         160

Gly Ile Ile Asp Ile Glu Phe Thr Arg Val Pro Cys Glu Phe Pro Gly
  165         170         175

Leu Lys Ile Gly Phe His Val Glu Glu Tyr Ser Lys Pro Arg Leu Leu
  180         185         190

Arg Gly Cys Trp Trp Ser Thr Arg Thr Ala Asn Gly Asp Val Val Gln
  195         200         205

Val Asp Leu Met Glu Ser Lys Thr Ala Arg Gly Pro Pro Thr Gly Arg
  210         215         220

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Trp	Ala	Pro	Met	Arg	Glu	Ser	Trp	Gly	Ser	Ile	Trp	Arg	Met	Asp	Thr
225					230					235					240
Asn	His	Arg	Met	Gln	Pro	Pro	Phe	Ser	Ile	Arg	Ile	Arg	Asn	Glu	Ser
				245					250					255	
Gly	Lys	Thr	Leu	Val	Ala	Arg	Asn	Val	Ile	Pro	Ala	Asn	Trp	Arg	Pro
			260					265					270		
Asn	Thr	Phe	Tyr	Arg	Ser	Phe	Val	Gln	Tyr	Ser					
	275						280								

<210> SEQ ID NO 12
 <211> LENGTH: 1389
 <212> TYPE: DNA
 <213> ORGANISM: Zea mays
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (272)...(1039)
 <223> OTHER INFORMATION: n = a, c, g, or t

<400> SEQUENCE: 12

ccacgcgtcc gcaagccaac aaccatcccc ctccctctcc ctccgtcagg ctgtcactgt	60
ccccctcacc gccgcccgtcc tcgtcaccac acctcaccgg ttgctcccac tccttccaga	120
accacctcct cgccaccgtg gctgacctgcc ctgcccgcta taagactctt cactcccgtc	180
gcgacgcagt cctcacaagc accagaccaa ttaactagct tcttctagct ctagctaggg	240
tcgtctgctg caagaaggta acagcgcagg c atg gag ggg aag gag gag gac	292
Met Glu Gly Lys Glu Glu Asp	
1 5	
gtc cgc ctg ggc gcc aac aag ttc tcg gag cgc cag ccc atc ggc acg	340
Val Arg Leu Gly Ala Asn Lys Phe Ser Glu Arg Gln Pro Ile Gly Thr	
10 15 20	
gcg gcg cag ggc acg gac gac aag gac tac aag gag ccc ccg ccg gcg	388
Ala Ala Gln Gly Thr Asp Asp Lys Asp Tyr Lys Glu Pro Pro Pro Ala	
25 30 35	
ccg ctc ttc gag ccc cgg gga gct caa gtc ctg gtc ctt cta ccg cgc	436
Pro Leu Phe Glu Pro Arg Gly Ala Gln Val Leu Val Leu Leu Pro Arg	
40 45 50 55	
cgg cat cgc cga gtt cgt cgc cac ctt cct ctt cct cta cat ctc cat	484
Arg His Arg Arg Val Arg Arg His Leu Pro Leu Pro Leu His Leu His	
60 65 70	
cct cac cgt cat ggg cgt ctc caa gtc cac ctc caa gtg cgc cac cgt	532
Pro His Arg His Gly Arg Leu Gln Val His Leu Gln Val Arg His Arg	
75 80 85	
cgg cat cca ggg cat cgc ctg gtc ctt cgg cgg cat gat ctt cgc cct	580
Arg His Pro Gly His Arg Leu Val Leu Arg Arg His Asp Leu Arg Pro	
90 95 100	
cgt cta ctg cac cgc cgg cat ctc cgg cgg gca cat caa ccc ggc ggt	628
Arg Leu Leu His Arg Arg His Leu Arg Arg Ala His Gln Pro Gly Gly	
105 110 115	
gac ctt cgg gct gtt cct ggc gag gaa gtt gtc cct cac cag ggc ggt	676
Asp Leu Arg Ala Val Pro Gly Glu Glu Val Val Pro His Gln Gly Gly	
120 125 130 135	
gtt tta cat cat cat gca gtg cct ggg cgc cat ctg cgg cgc ggg cgt	724
Val Leu His His His Ala Val Pro Gly Arg His Leu Arg Arg Gly Arg	
140 145 150	
cgt caa ggg gtt cca gca ggg gct gta cat ggg caa cgg cgg cgg cgc	772
Arg Gln Gly Val Pro Ala Gly Ala Val His Gly Gln Arg Arg Arg Arg	
155 160 165	
caa cgt cgt ggc gcc cgg cta cac caa ggg cga cgg cct agg cgc cga	820
Gln Arg Arg Gly Ala Arg Leu His Gln Gly Arg Arg Pro Arg Arg Arg	
170 175 180	

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gat cgt cgg cac ctt cat cct cgt cta cac cgt ctt ctc cgc cac cga      868
Asp Arg Arg His Leu His Pro Arg Leu His Arg Leu Leu Arg His Arg
    185                190                195

cgc caa gag gaa cgc cag gga ctc cca tgt gcc gat cct cgc ccc tct      916
Arg Gln Glu Glu Arg Gln Gly Leu Pro Cys Ala Asp Pro Arg Pro Ser
    200                205                210                215

tcc aat cgg gtt tgc cgt gtt cct cgt cca cct ggc cac cat ccc tat      964
Ser Asn Arg Val Cys Arg Val Pro Arg Pro Pro Gly His His Pro Tyr
                220                225                230

cac cgg cac cgg cat caa ccc cgc gcg gag cct tgg cgc cgc cgt aat      1012
His Arg His Arg His Gln Pro Arg Ala Glu Pro Trp Arg Arg Arg Asn
                235                240                245

tta caa cca gca cca tgc gtg ggc tga ccaactggatc ttctgggtcg          1059
Leu Gln Pro Ala Pro Cys Val Gly *
    250                255

gcccttcat cggcgctgcg ctggctgccca tctaccacca ggtgatcatc agggcgatcc  1119

cgttcaagag taggtcttaa aggagccgat getgctgctt cgagatgctg ccggtcttga  1179

aaggatggat tcgtggctgt ttcaaatgat ccctactat gttacgtgga gttccattcc  1239

tctttcaaag ttcggagctg cttttatccg aaccagact tgtaattcat ctgtaccaat  1299

tgtgtaatat gccgcgcctc tgttatgtgc aattcaaat tatgagacag cgagtcaagc  1359

ttaaagagtt canaaaaaaaa aaaaaaaaaa                                1389
    
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<210> SEQ ID NO 13
<211> LENGTH: 255
<212> TYPE: PRT
<213> ORGANISM: Zea mays
<220> FEATURE:
<223> OTHER INFORMATION: Xaa = any amino acid
    
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<400> SEQUENCE: 13
    
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Met Glu Gly Lys Glu Glu Asp Val Arg Leu Gly Ala Asn Lys Phe Ser
  1                    5                10                15

Glu Arg Gln Pro Ile Gly Thr Ala Ala Gln Gly Thr Asp Asp Lys Asp
                20                25                30

Tyr Lys Glu Pro Pro Pro Ala Pro Leu Phe Glu Pro Arg Gly Ala Gln
    35                40                45

Val Leu Val Leu Leu Pro Arg Arg His Arg Arg Val Arg Arg His Leu
    50                55                60

Pro Leu Pro Leu His Leu His Pro His Arg His Gly Arg Leu Gln Val
    65                70                75                80

His Leu Gln Val Arg His Arg Arg His Pro Gly His Arg Leu Val Leu
                85                90                95

Arg Arg His Asp Leu Arg Pro Arg Leu Leu His Arg Arg His Leu Arg
    100                105                110

Arg Ala His Gln Pro Gly Gly Asp Leu Arg Ala Val Pro Gly Glu Glu
    115                120                125

Val Val Pro His Gln Gly Gly Val Leu His His His Ala Val Pro Gly
    130                135                140

Arg His Leu Arg Arg Gly Arg Arg Gln Gly Val Pro Ala Gly Ala Val
    145                150                155                160

His Gly Gln Arg Arg Arg Arg Gln Arg Arg Gly Ala Arg Leu His Gln
                165                170                175

Gly Arg Arg Pro Arg Arg Arg Asp Arg Arg His Leu His Pro Arg Leu
    180                185                190
    
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His Arg Leu Leu Arg His Arg Arg Gln Glu Glu Arg Gln Gly Leu Pro
 195 200 205
 Cys Ala Asp Pro Arg Pro Ser Ser Asn Arg Val Cys Arg Val Pro Arg
 210 215 220
 Pro Pro Gly His His Pro Tyr His Arg His Arg His Gln Pro Arg Ala
 225 230 235 240
 Glu Pro Trp Arg Arg Arg Asn Leu Gln Pro Ala Pro Cys Val Gly
 245 250 255

<210> SEQ ID NO 14
 <211> LENGTH: 1238
 <212> TYPE: DNA
 <213> ORGANISM: Zea mays
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (227)...(976)
 <223> OTHER INFORMATION: n = a, c, g, or t

<400> SEQUENCE: 14

aaatgttttg tgacgattat ccccgaccgcg tccagagtac tctaaccac aagttgaggc 60
 ncgccctgcag cccatcagac gaggacgcgc gcgtgtataa aagctgactg gactcccagc 120
 gtctgtcagc gaancgaagc agcagccaat tcgctcgagt tcagatcgag cgcgcgccaa 180
 gcaagtcttc cggccggccg cgaagagcgc aatcaagcaa gacaag atg gtg aag 235
 Met Val Lys
 1
 ctc gcc ttc gga agc gtc ggc gac tcc ttc agc gcc acc tcc atc aag 283
 Leu Ala Phe Gly Ser Val Gly Asp Ser Phe Ser Ala Thr Ser Ile Lys
 5 10 15
 gcc tac gtg gcc gag ttc atc gcc acc ctc ctc ttc gtc ttc gcc ggc 331
 Ala Tyr Val Ala Glu Phe Ile Ala Thr Leu Leu Phe Val Phe Ala Gly
 20 25 30 35
 gtc ggt tcc gcc atc gcc tac ggg caa ctg acg aat ggc ggc gcg ctg 379
 Val Gly Ser Ala Ile Ala Tyr Gly Gln Leu Thr Asn Gly Gly Ala Leu
 40 45 50
 gac ccg gcg ggc ctg gtg gcg atc gcg atc gcg cac gcg ctg gcg ctg 427
 Asp Pro Ala Gly Leu Val Ala Ile Ala Ile Ala His Ala Leu Ala Leu
 55 60 65
 ttc gtg ggc gtg tcc gtc gcg gcg aac atc tcg ggc ggc cac ctg aac 475
 Phe Val Gly Val Ser Val Ala Ala Asn Ile Ser Gly Gly His Leu Asn
 70 75 80
 ccg gcc gtg acg ttc ggg ctg gcc gtg ggc ggc cac atc acc atc ctg 523
 Pro Ala Val Thr Phe Gly Leu Ala Val Gly Gly His Ile Thr Ile Leu
 85 90 95
 acg ggc gtc ttc tac tgg gtg gcc cag ctg ctg ggc gcc acc gtg gcg 571
 Thr Gly Val Phe Tyr Trp Val Ala Gln Leu Leu Gly Ala Thr Val Ala
 100 105 110 115
 tgc ctg ctc ctc ggg ttc gtc acc cac ggc aag gcc atc ccg acg cac 619
 Cys Leu Leu Leu Gly Phe Val Thr His Gly Lys Ala Ile Pro Thr His
 120 125 130
 gcc gtc gcg ggc atc agc gag ctg gaa ggc gtc gtg ttc gag gtc gtc 667
 Ala Val Ala Gly Ile Ser Glu Leu Glu Gly Val Val Phe Glu Val Val
 135 140 145
 atc acc ttc gcg ctc gtc tac acc gtg tac gcc acc gcc gcc gac ccc 715
 Ile Thr Phe Ala Leu Val Tyr Thr Val Tyr Ala Thr Ala Ala Asp Pro
 150 155 160
 aag aag ggc tcg ctc ggc acc atc gcg ccc atc gcc atc ggc ttc atc 763
 Lys Lys Gly Ser Leu Gly Thr Ile Ala Pro Ile Ala Ile Gly Phe Ile
 165 170 175
 gtc ggc gcc aac atc ctc gcc gcg ggg ccc ttc agc ggc ggc tcc atg 811

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Val Gly Ala Asn Ile Leu Ala Ala Gly Pro Phe Ser Gly Gly Ser Met	
180	185 190 195
aac ccc gcc cgc tcc ttc ggc ccc gcc gtc gcc gcg ggc gac ttc gcc	859
Asn Pro Ala Arg Ser Phe Gly Pro Ala Val Ala Ala Gly Asp Phe Ala	
200	205 210
gga aac tgg gtc tac tgg gtc ggc ccg ctc gtc ggc ggc ggc ctc gct	907
Gly Asn Trp Val Tyr Trp Val Gly Pro Leu Val Gly Gly Gly Leu Ala	
215	220 225
ggc ctc gtc tac ggc gac gtc ttc att ggc ggc tcc tac cag cag gtc	955
Gly Leu Val Tyr Gly Asp Val Phe Ile Gly Gly Ser Tyr Gln Gln Val	
230	235 240
gcg gac cag gac tac gcc taa tttattcacc actccatctc cgctctggat	1006
Ala Asp Gln Asp Tyr Ala *	
245	
gaatggattc aaaaccgtcg tcgtttgctt ttgctcctcg ccacgttcaa ttaatggttg	1066
tgtatgcatg tatgtgcaa tatgatgtgc cttgcccctg gtccattcat ttccccttct	1126
tttttcgggg tgaatagat gtaaagatct cgtcttgccct gccgtactcg cgctgtgttg	1186
ggaaaaattg gttttcgctc caagtttgct tacgcaaaga aaaaaaaaa aa	1238

<210> SEQ ID NO 15
 <211> LENGTH: 249
 <212> TYPE: PRT
 <213> ORGANISM: Zea mays
 <220> FEATURE:
 <223> OTHER INFORMATION: Xaa = any amino acid

<400> SEQUENCE: 15

Met Val Lys Leu Ala Phe Gly Ser Val Gly Asp Ser Phe Ser Ala Thr	
1	5 10 15
Ser Ile Lys Ala Tyr Val Ala Glu Phe Ile Ala Thr Leu Leu Phe Val	
20	25 30
Phe Ala Gly Val Gly Ser Ala Ile Ala Tyr Gly Gln Leu Thr Asn Gly	
35	40 45
Gly Ala Leu Asp Pro Ala Gly Leu Val Ala Ile Ala Ile Ala His Ala	
50	55 60
Leu Ala Leu Phe Val Gly Val Ser Val Ala Ala Asn Ile Ser Gly Gly	
65	70 75 80
His Leu Asn Pro Ala Val Thr Phe Gly Leu Ala Val Gly Gly His Ile	
85	90 95
Thr Ile Leu Thr Gly Val Phe Tyr Trp Val Ala Gln Leu Leu Gly Ala	
100	105 110
Thr Val Ala Cys Leu Leu Leu Gly Phe Val Thr His Gly Lys Ala Ile	
115	120 125
Pro Thr His Ala Val Ala Gly Ile Ser Glu Leu Glu Gly Val Val Phe	
130	135 140
Glu Val Val Ile Thr Phe Ala Leu Val Tyr Thr Val Tyr Ala Thr Ala	
145	150 155 160
Ala Asp Pro Lys Lys Gly Ser Leu Gly Thr Ile Ala Pro Ile Ala Ile	
165	170 175
Gly Phe Ile Val Gly Ala Asn Ile Leu Ala Ala Gly Pro Phe Ser Gly	
180	185 190
Gly Ser Met Asn Pro Ala Arg Ser Phe Gly Pro Ala Val Ala Ala Gly	
195	200 205
Asp Phe Ala Gly Asn Trp Val Tyr Trp Val Gly Pro Leu Val Gly Gly	
210	215 220

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Gly Leu Ala Gly Leu Val Tyr Gly Asp Val Phe Ile Gly Gly Ser Tyr
225 230 235 240

Gln Gln Val Ala Asp Gln Asp Tyr Ala
245

<210> SEQ ID NO 16
<211> LENGTH: 1170
<212> TYPE: DNA
<213> ORGANISM: Zea mays
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (593)...(769)

<400> SEQUENCE: 16

gtccattcca atctcatctc aaatctgtcc atgggctgac aagaccgcg cctgaaaaca 60
tttgcggtggg ggctgctgca cgcagctggg cgcggagttc gtgggcacgt tcatcctcat 120
cttcttcgcg acggcggcgc cgatcgtgaa ccagaagtac ggcggcgcga tcagcccgtt 180
cgggaacgcg gcgctgcgcgg ggctggcggg ggcgaccgtg atcctgtcga cggggcacat 240
ctccggggcg cacctgaacc cgtcgtcac catcgccttc gcggcgctgc gccacttccc 300
ctggctgcag gtgcccgtg acgtggcctg ccaggcgtg gcacccgtct gcgcccctt 360
cgcgctcaag ggcgtcttcc acccgttcct ctccggcggc gtcaccgtgc cgcagccac 420
cgtctccacc gccaggcgt tcttcaccga gttcatcctc tccttcaacc tcctcttctg 480
cgtcaccgcc gtcgccaccg acaccgcgc agtgggtgaa ctgcccggga tcgcccgtgg 540
agcggccgta acgctgaaca tcctcgtcgc cgggcccagc acgggcccgt cc atg aac 598
Met Asn
1
ccg gtg agg acg ctg ggg ccg gcc gtg gcg gcg ggg aac tac cgg cag 646
Pro Val Arg Thr Leu Gly Pro Ala Val Ala Ala Gly Asn Tyr Arg Gln
5 10 15
ctc tgg atc tac ctg ctg gcc ccg acg ctg ggc gcg ttg gcg ggg gcc 694
Leu Trp Ile Tyr Leu Leu Ala Pro Thr Leu Gly Ala Leu Ala Gly Ala
20 25 30
agc gtg tac aag gcg gtg aag ctc agg gac gag aac ggt gag acg ccg 742
Ser Val Tyr Lys Ala Val Lys Leu Arg Asp Glu Asn Gly Glu Thr Pro
35 40 45 50
cgc acg cag cgc agc ttc cgc cgc tga cgacgcacac tggccacggg 789
Arg Thr Gln Arg Ser Phe Arg Arg *
55
cgcgagacat tgtccggccg tgtcacgcac gcccgctcc tcctccgcc cgcgtaacg 849
cacggccacg acgtgtccgc ggctgtacgt gctgtgtctg tgtgtaccaa taaataagcc 909
ccgttttctg tctccagaa cggctccagt ctatgtgtac gtggtctgtg ttgtgatttg 969
cgaattggat tattgtgggt cgtctcgtcg aggtctctcg ggtgtcgggt gggctctgatg 1029
cgatccatca gcgtcgtgtc cgaataaaaag ccacgccgat gcgcccgtg acgggcatct 1089
ggatgtgtga tttctgaaca agatttgctt aatttcactt gcttaaaaaa aaaaaaaaaa 1149
aaaaaaaaaa aaaaaaaaaa a 1170

<210> SEQ ID NO 17
<211> LENGTH: 58
<212> TYPE: PRT
<213> ORGANISM: Zea mays

<400> SEQUENCE: 17

Met Asn Pro Val Arg Thr Leu Gly Pro Ala Val Ala Ala Gly Asn Tyr
1 5 10 15

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Arg Gln Leu Trp Ile Tyr Leu Leu Ala Pro Thr Leu Gly Ala Leu Ala
 20 25 30

Gly Ala Ser Val Tyr Lys Ala Val Lys Leu Arg Asp Glu Asn Gly Glu
 35 40 45

Thr Pro Arg Thr Gln Arg Ser Phe Arg Arg
 50 55

<210> SEQ ID NO 18
 <211> LENGTH: 1557
 <212> TYPE: DNA
 <213> ORGANISM: Zea mays
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1) ... (1557)

<400> SEQUENCE: 18

atg gct cgt ggc gac ggc ggg cag ctg gcg gag ctg tcc gcg ggg gtc 48
 Met Ala Arg Gly Asp Gly Gly Gln Leu Ala Glu Leu Ser Ala Gly Val
 1 5 10 15

cgc ggc gcg gcc gcg gtg gtg gac cac gtg gcc ccg atc agc ctc ggg 96
 Arg Gly Ala Ala Ala Val Val Asp His Val Ala Pro Ile Ser Leu Gly
 20 25 30

agg ctc atc ctc gcc ggc atg gtc gcc ggc ggc gtg cag tac ggc tgg 144
 Arg Leu Ile Leu Ala Gly Met Val Ala Gly Gly Val Gln Tyr Gly Trp
 35 40 45

gcg ctg cag ctc tcc ctc ctc acg ccc tac gtg cag act ctg ggg ctt 192
 Ala Leu Gln Leu Ser Leu Leu Thr Pro Tyr Val Gln Thr Leu Gly Leu
 50 55 60

tca cat gcg ctc act tca ttc atg tgg ctc tgc ggc cct att gcc ggc 240
 Ser His Ala Leu Thr Ser Phe Met Trp Leu Cys Gly Pro Ile Ala Gly
 65 70 75 80

tta gtg gtc caa ccg ctg gtt ggc ctg tac agc gac agg tgt aca tcg 288
 Leu Val Val Gln Pro Leu Val Gly Leu Tyr Ser Asp Arg Cys Thr Ser
 85 90 95

aga tgg ggg aga cgg agg ccg ttt atc ctg aca ggg tgc atg ctc atc 336
 Arg Trp Gly Arg Arg Arg Pro Phe Ile Leu Thr Gly Cys Met Leu Ile
 100 105 110

tgc gtt gcc gtc att gtt gtc gga ttc tcg tca gac atc gga gct gct 384
 Cys Val Ala Val Ile Val Val Gly Phe Ser Ser Asp Ile Gly Ala Ala
 115 120 125

cta ggg gac acg aag gaa cac tgc agc ctc tac cac ggt cct cgt tgg 432
 Leu Gly Asp Thr Lys Glu His Cys Ser Leu Tyr His Gly Pro Arg Trp
 130 135 140

cac gct gcg atc gtg tac gtt ctg ggg ttt tgg ctc ctt gac ttc tcc 480
 His Ala Ala Ile Val Tyr Val Leu Gly Phe Trp Leu Leu Asp Phe Ser
 145 150 155 160

aac aac act gtg cag ggt cca gca cgt gct atg atg gct gat cta tgt 528
 Asn Asn Thr Val Gln Gly Pro Ala Arg Ala Met Met Ala Asp Leu Cys
 165 170 175

gac cat cat ggg cca agt gcg gct aac tcc atc ttc tgt tct tgg atg 576
 Asp His His Gly Pro Ser Ala Ala Asn Ser Ile Phe Cys Ser Trp Met
 180 185 190

gcg ctg gga aac atc cta ggc tac tcc tct ggc tcc acg aac aat tgg 624
 Ala Leu Gly Asn Ile Leu Gly Tyr Ser Ser Gly Ser Thr Asn Asn Trp
 195 200 205

cac aag tgg ttt ccc ttc ctt aaa acg agc gcc tgc tgt gag gcc tgt 672
 His Lys Trp Phe Pro Phe Leu Lys Thr Ser Ala Cys Cys Glu Ala Cys
 210 215 220

gcg aac ctg aaa ggt gca ttt ctg gtg gcc gtg gtg ttc cta gtc ctg 720
 Ala Asn Leu Lys Gly Ala Phe Leu Val Ala Val Val Phe Leu Val Leu

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225	230	235	240	
tgc ctg acg gta acc ctg atc ttc gcc aag gag gtg ccg tac aga gcg				768
Cys Leu Thr Val Thr Leu Ile Phe Ala Lys Glu Val Pro Tyr Arg Ala	245	250	255	
aac gag aac ctc ccg acg acg aag gcc ggc ggc gag gtc gag act gag				816
Asn Glu Asn Leu Pro Thr Thr Lys Ala Gly Gly Glu Val Glu Thr Glu	260	265	270	
cct acc ggg cca ctt gcc gtg ctc aag ggc ttc aag gac ctg cct ccc				864
Pro Thr Gly Pro Leu Ala Val Leu Lys Gly Phe Lys Asp Leu Pro Pro	275	280	285	
ggg atg ccg tcc gtg ctc ctc gtg act gcc atc acc tgg ctt tcg tgg				912
Gly Met Pro Ser Val Leu Leu Val Thr Ala Ile Thr Trp Leu Ser Trp	290	295	300	
ttc ccg ttc atc ctc tac gac acc gac tgg atg ggc cgg gag atc tac				960
Phe Pro Phe Ile Leu Tyr Asp Thr Asp Trp Met Gly Arg Glu Ile Tyr	305	310	315	320
cac ggc gac ccc aag ggg agc aac gcc cag atc tcg gcg ttc aac gaa				1008
His Gly Asp Pro Lys Gly Ser Asn Ala Gln Ile Ser Ala Phe Asn Glu	325	330	335	
ggt gtc cga gtc ggc gcg ttc ggg ctg cta ctc aac tcg gtt att cta				1056
Gly Val Arg Val Gly Ala Phe Gly Leu Leu Leu Asn Ser Val Ile Leu	340	345	350	
ggg ttc agc tcg ttc ctg atc gag ccc atg tgc cgg aag gtc ggg ccg				1104
Gly Phe Ser Ser Phe Leu Ile Glu Pro Met Cys Arg Lys Val Gly Pro	355	360	365	
agg gtg gtg tgg gtg acg agc aac ttc atg gtc tgc gtc gcc atg gcg				1152
Arg Val Val Trp Val Thr Ser Asn Phe Met Val Cys Val Ala Met Ala	370	375	380	
gcc acc gcg ctg atc agc ttc tgg tcg ctc agg gac tac cac ggg tac				1200
Ala Thr Ala Leu Ile Ser Phe Trp Ser Leu Arg Asp Tyr His Gly Tyr	385	390	395	400
gtg cag gac gcc atc acc gcg aac gcc agc atc aag gcc gtc tgc ctc				1248
Val Gln Asp Ala Ile Thr Ala Asn Ala Ser Ile Lys Ala Val Cys Leu	405	410	415	
gtc ctc ttc gcc ttc ctg ggc gtc cct ctc gcc atc ctg tac agc gtc				1296
Val Leu Phe Ala Phe Leu Gly Val Pro Leu Ala Ile Leu Tyr Ser Val	420	425	430	
ccg ttc gcg gtg acg gcg cag ctg gcg gcc acc ccg ggc ggc ggg cag				1344
Pro Phe Ala Val Thr Ala Gln Leu Ala Ala Thr Arg Gly Gly Gly Gln	435	440	445	
ggg ctg tgc acc ggc gtc ctc aac atc tcc atc gtc atc cct cag gtg				1392
Gly Leu Cys Thr Gly Val Leu Asn Ile Ser Ile Val Ile Pro Gln Val	450	455	460	
atc atc gcg ctg ggc gcc ggc ccg tgg gac gcg ctg ttc ggg aag ggc				1440
Ile Ile Ala Leu Gly Ala Gly Pro Trp Asp Ala Leu Phe Gly Lys Gly	465	470	475	480
aac atc ccg gcg ttc ggc gtc gcg tcg gcc ttc gcc ctc gtc ggc ggc				1488
Asn Ile Pro Ala Phe Gly Val Ala Ser Ala Phe Ala Leu Val Gly Gly	485	490	495	
gtc gtg ggc gtg ttc ctg ctg ccc aag atc tcc aag cgc cag ttc ccg				1536
Val Val Gly Val Phe Leu Leu Pro Lys Ile Ser Lys Arg Gln Phe Arg	500	505	510	
gcc gtc agc gcg ggc ggc cac				1557
Ala Val Ser Ala Gly Gly His	515			

<210> SEQ ID NO 19

<211> LENGTH: 519

<212> TYPE: PRT

<213> ORGANISM: Zea mays

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<400> SEQUENCE: 19

Met Ala Arg Gly Asp Gly Gly Gln Leu Ala Glu Leu Ser Ala Gly Val
 1 5 10 15
 Arg Gly Ala Ala Ala Val Val Asp His Val Ala Pro Ile Ser Leu Gly
 20 25 30
 Arg Leu Ile Leu Ala Gly Met Val Ala Gly Gly Val Gln Tyr Gly Trp
 35 40 45
 Ala Leu Gln Leu Ser Leu Leu Thr Pro Tyr Val Gln Thr Leu Gly Leu
 50 55 60
 Ser His Ala Leu Thr Ser Phe Met Trp Leu Cys Gly Pro Ile Ala Gly
 65 70 75 80
 Leu Val Val Gln Pro Leu Val Gly Leu Tyr Ser Asp Arg Cys Thr Ser
 85 90 95
 Arg Trp Gly Arg Arg Arg Pro Phe Ile Leu Thr Gly Cys Met Leu Ile
 100 105 110
 Cys Val Ala Val Ile Val Val Gly Phe Ser Ser Asp Ile Gly Ala Ala
 115 120 125
 Leu Gly Asp Thr Lys Glu His Cys Ser Leu Tyr His Gly Pro Arg Trp
 130 135 140
 His Ala Ala Ile Val Tyr Val Leu Gly Phe Trp Leu Leu Asp Phe Ser
 145 150 155 160
 Asn Asn Thr Val Gln Gly Pro Ala Arg Ala Met Met Ala Asp Leu Cys
 165 170 175
 Asp His His Gly Pro Ser Ala Ala Asn Ser Ile Phe Cys Ser Trp Met
 180 185 190
 Ala Leu Gly Asn Ile Leu Gly Tyr Ser Ser Gly Ser Thr Asn Asn Trp
 195 200 205
 His Lys Trp Phe Pro Phe Leu Lys Thr Ser Ala Cys Cys Glu Ala Cys
 210 215 220
 Ala Asn Leu Lys Gly Ala Phe Leu Val Ala Val Val Phe Leu Val Leu
 225 230 235 240
 Cys Leu Thr Val Thr Leu Ile Phe Ala Lys Glu Val Pro Tyr Arg Ala
 245 250 255
 Asn Glu Asn Leu Pro Thr Thr Lys Ala Gly Gly Glu Val Glu Thr Glu
 260 265 270
 Pro Thr Gly Pro Leu Ala Val Leu Lys Gly Phe Lys Asp Leu Pro Pro
 275 280 285
 Gly Met Pro Ser Val Leu Leu Val Thr Ala Ile Thr Trp Leu Ser Trp
 290 295 300
 Phe Pro Phe Ile Leu Tyr Asp Thr Asp Trp Met Gly Arg Glu Ile Tyr
 305 310 315 320
 His Gly Asp Pro Lys Gly Ser Asn Ala Gln Ile Ser Ala Phe Asn Glu
 325 330 335
 Gly Val Arg Val Gly Ala Phe Gly Leu Leu Leu Asn Ser Val Ile Leu
 340 345 350
 Gly Phe Ser Ser Phe Leu Ile Glu Pro Met Cys Arg Lys Val Gly Pro
 355 360 365
 Arg Val Val Trp Val Thr Ser Asn Phe Met Val Cys Val Ala Met Ala
 370 375 380
 Ala Thr Ala Leu Ile Ser Phe Trp Ser Leu Arg Asp Tyr His Gly Tyr
 385 390 395 400
 Val Gln Asp Ala Ile Thr Ala Asn Ala Ser Ile Lys Ala Val Cys Leu

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405				410				415								
Val	Leu	Phe	Ala	Phe	Leu	Gly	Val	Pro	Leu	Ala	Ile	Leu	Tyr	Ser	Val	
			420						425				430			
Pro	Phe	Ala	Val	Thr	Ala	Gln	Leu	Ala	Ala	Thr	Arg	Gly	Gly	Gly	Gln	
		435					440					445				
Gly	Leu	Cys	Thr	Gly	Val	Leu	Asn	Ile	Ser	Ile	Val	Ile	Pro	Gln	Val	
	450					455					460					
Ile	Ile	Ala	Leu	Gly	Ala	Gly	Pro	Trp	Asp	Ala	Leu	Phe	Gly	Lys	Gly	
465					470					475					480	
Asn	Ile	Pro	Ala	Phe	Gly	Val	Ala	Ser	Ala	Phe	Ala	Leu	Val	Gly	Gly	
			485						490					495		
Val	Val	Gly	Val	Phe	Leu	Leu	Pro	Lys	Ile	Ser	Lys	Arg	Gln	Phe	Arg	
			500						505				510			
Ala	Val	Ser	Ala	Gly	Gly	His										
			515													
<210> SEQ ID NO 20																
<211> LENGTH: 2022																
<212> TYPE: DNA																
<213> ORGANISM: Zea mays																
<220> FEATURE:																
<221> NAME/KEY: CDS																
<222> LOCATION: (1)...(2022)																
<400> SEQUENCE: 20																
atg	gag	acc	cgg	gac	acg	gat	gcg	acg	ccg	ctc	ccc	tac	tcg	tac	acg	48
Met	Glu	Thr	Arg	Asp	Thr	Asp	Ala	Thr	Pro	Leu	Pro	Tyr	Ser	Tyr	Thr	
1				5					10					15		
ccg	ctg	ccg	gcc	gcc	gac	gcc	gcg	tcg	gcc	gag	gtc	tcc	ggc	acc	ggc	96
Pro	Leu	Pro	Ala	Ala	Asp	Ala	Ala	Ser	Ala	Glu	Val	Ser	Gly	Thr	Gly	
			20						25				30			
agg	acg	cgg	agc	agg	cgg	cgg	ccc	ctc	tgc	gcg	gcg	gcg	ctc	gtg	ctc	144
Arg	Thr	Arg	Ser	Arg	Arg	Arg	Pro	Leu	Cys	Ala	Ala	Ala	Leu	Val	Leu	
		35					40					45				
tcc	gcc	gcg	ctg	ctc	cta	gcc	gtg	gcc	gcg	ctc	gtc	ggc	gtc	ggg	agc	192
Ser	Ala	Ala	Leu	Leu	Leu	Ala	Val	Ala	Ala	Leu	Val	Gly	Val	Gly	Ser	
	50					55				60						
cgg	ccc	ggc	gcg	gtg	ggg	atg	aca	gag	tcg	gcg	gcc	tcg	tcg	ccg	acg	240
Arg	Pro	Gly	Ala	Val	Gly	Met	Thr	Glu	Ser	Ala	Ala	Ser	Ser	Pro	Thr	
65				70					75					80		
ccg	agc	agg	agc	agg	ggc	ccc	gag	gcc	ggc	gtg	tcc	gag	aag	acg	tcc	288
Pro	Ser	Arg	Ser	Arg	Gly	Pro	Glu	Ala	Gly	Val	Ser	Glu	Lys	Thr	Ser	
			85						90					95		
ggc	gcg	tct	gac	gac	ggc	ggc	agg	ctc	cgt	gga	gcc	ggc	ggg	aac	gcc	336
Gly	Ala	Ser	Asp	Asp	Gly	Gly	Arg	Leu	Arg	Gly	Ala	Gly	Gly	Asn	Ala	
			100						105				110			
ttc	ccg	tgg	agc	aat	gcg	atg	ctg	cag	tgg	cag	cgc	acg	gga	ttc	cac	384
Phe	Pro	Trp	Ser	Asn	Ala	Met	Leu	Gln	Trp	Gln	Arg	Thr	Gly	Phe	His	
		115					120					125				
ttc	cag	ccg	cag	aag	aac	tgg	atg	aac	gac	ccc	aat	ggc	ccc	gtg	tac	432
Phe	Gln	Pro	Gln	Lys	Asn	Trp	Met	Asn	Asp	Pro	Asn	Gly	Pro	Val	Tyr	
		130				135				140						
tac	aag	ggc	tgg	tac	cac	ctc	ttc	tac	cag	tac	aac	cct	gac	ggc	gcc	480
Tyr	Lys	Gly	Trp	Tyr	His	Leu	Phe	Tyr	Gln	Tyr	Asn	Pro	Asp	Gly	Ala	
145					150					155				160		
atc	tgg	ggc	aac	aag	atc	gcg	tgg	ggc	cac	gcc	gtg	tcc	cgc	gac	ctg	528
Ile	Trp	Gly	Asn	Lys	Ile	Ala	Trp	Gly	His	Ala	Val	Ser	Arg	Asp	Leu	
			165						170					175		
atc	cgc	tgg	cgc	cgc	ctc	ccg	ctg	gcc	atg	gtg	ccc	gac	cag	tgg	tac	576

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Ile	Arg	Trp	Arg	Arg	Leu	Pro	Leu	Ala	Met	Val	Pro	Asp	Gln	Trp	Tyr	
			180					185					190			
gac	acc	aac	ggc	gtg	tgg	acg	ggg	tcc	gcc	acc	acg	ctc	ccc	gac	ggc	624
Asp	Thr	Asn	Gly	Val	Trp	Thr	Gly	Ser	Ala	Thr	Thr	Leu	Pro	Asp	Gly	
		195					200					205				
cgc	ctc	gca	atg	ctc	tac	agg	ggc	tcc	acc	aac	gcc	tcc	gtc	cag	gtg	672
Arg	Leu	Ala	Met	Leu	Tyr	Arg	Gly	Ser	Thr	Asn	Ala	Ser	Val	Gln	Val	
	210					215					220					
cag	tgc	ctg	gcc	gtg	ccc	gcc	gac	gac	gcc	gac	ccg	ctg	ctc	acc	aac	720
Gln	Cys	Leu	Ala	Val	Pro	Ala	Asp	Asp	Ala	Asp	Pro	Leu	Leu	Thr	Asn	
225					230					235					240	
tgg	acc	aag	tac	gag	ggc	aac	ccg	gtg	ctg	tac	ccg	ccc	ccg	ggc	atc	768
Trp	Thr	Lys	Tyr	Glu	Gly	Asn	Pro	Val	Leu	Tyr	Pro	Pro	Pro	Gly	Ile	
				245					250					255		
ggg	ccc	aag	gac	ttc	cgc	gac	ccc	acc	acg	gtc	tgg	atc	gac	ccc	tcg	816
Gly	Pro	Lys	Asp	Phe	Arg	Asp	Pro	Thr	Thr	Val	Trp	Ile	Asp	Pro	Ser	
			260					265					270			
gac	ggc	gca	tgg	cgc	gtc	gtc	atc	ggc	tcc	aag	gac	gac	gac	ggc	cac	864
Asp	Gly	Ala	Trp	Arg	Val	Val	Ile	Gly	Ser	Lys	Asp	Asp	Asp	Gly	His	
		275					280						285			
gcg	ggc	atc	gcc	gtc	gtc	tac	cgc	acc	acg	gac	ctg	gtg	cac	ttc	gag	912
Ala	Gly	Ile	Ala	Val	Val	Tyr	Arg	Thr	Thr	Asp	Leu	Val	His	Phe	Glu	
	290					295					300					
ctc	ctc	ccg	ggc	ctg	ctg	cac	cgc	gtc	gac	ggc	acc	ggc	atg	tgg	gag	960
Leu	Leu	Pro	Gly	Leu	Leu	His	Arg	Val	Asp	Gly	Thr	Gly	Met	Trp	Glu	
305					310					315					320	
tgc	atc	gac	ttc	tac	ccc	gtc	gcc	aca	cga	ggc	agg	gcg	tcg	gcc	aac	1008
Cys	Ile	Asp	Phe	Tyr	Pro	Val	Ala	Thr	Arg	Gly	Arg	Ala	Ser	Ala	Asn	
				325					330					335		
ggc	gtc	gac	atg	tcc	gac	gcc	atc	gcc	agc	aac	gga	gcc	gtc	gcc	ggg	1056
Gly	Val	Asp	Met	Ser	Asp	Ala	Ile	Ala	Ser	Asn	Gly	Ala	Val	Ala	Gly	
			340					345					350			
gac	gtc	ctg	cac	gtc	atg	aag	gcc	agc	atg	gac	gac	gac	cgc	cac	gac	1104
Asp	Val	Leu	His	Val	Met	Lys	Ala	Ser	Met	Asp	Asp	Asp	Arg	His	Asp	
		355					360						365			
tac	tac	gcg	ctg	ggg	agg	tac	gac	gcg	gcc	gcc	aac	gcc	tgg	acg	ccg	1152
Tyr	Tyr	Ala	Leu	Gly	Arg	Tyr	Asp	Ala	Ala	Ala	Asn	Ala	Trp	Thr	Pro	
		370				375					380					
atc	gac	gcc	ggc	agg	gac	gtc	ggc	atc	ggc	ctg	cgc	tac	gac	tgg	ggc	1200
Ile	Asp	Ala	Gly	Arg	Asp	Val	Gly	Ile	Gly	Leu	Arg	Tyr	Asp	Trp	Gly	
385					390					395					400	
aag	ttc	tac	gcg	tcc	aag	acg	ttc	tac	gac	ccg	gcc	aag	cgc	cgc	cgc	1248
Lys	Phe	Tyr	Ala	Ser	Lys	Thr	Phe	Tyr	Asp	Pro	Ala	Lys	Arg	Arg	Arg	
				405					410					415		
gtg	ctg	tgg	gga	tgg	gtc	ggc	gag	aca	gac	tcg	gag	cgc	gcg	gac	gtg	1296
Val	Leu	Trp	Gly	Trp	Val	Gly	Glu	Thr	Asp	Ser	Glu	Arg	Ala	Asp	Val	
			420					425					430			
tcc	aag	gga	tgg	gcg	tcg	ctg	cag	ggt	atc	ccc	cgg	acg	gtg	ctc	ctg	1344
Ser	Lys	Gly	Trp	Ala	Ser	Leu	Gln	Gly	Ile	Pro	Arg	Thr	Val	Leu	Leu	
		435					440					445				
gac	acc	aag	acg	ggc	agc	aac	ctg	ctt	cag	tgg	ccc	gtg	gag	gag	gtg	1392
Asp	Thr	Lys	Thr	Gly	Ser	Asn	Leu	Leu	Gln	Trp	Pro	Val	Glu	Glu	Val	
		450				455					460					
gag	acg	ctg	cgc	acc	aac	tcc	acc	gac	ctc	agc	ggc	atc	acc	atc	gac	1440
Glu	Thr	Leu	Arg	Thr	Asn	Ser	Thr	Asp	Leu	Ser	Gly	Ile	Thr	Ile	Asp	
465					470					475					480	
tac	ggc	tcc	gtg	ttc	ccg	ctc	aac	ctc	cgc	cgc	gcc	acc	cag	ctg	gac	1488
Tyr	Gly	Ser	Val	Phe	Pro	Leu	Asn	Leu	Arg	Arg	Ala	Thr	Gln	Leu	Asp	
				485					490					495		

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atc gag gcg gag ttc cag ctg gac cgc cgc gcc gtc atg tcg ctc aac	1536
Ile Glu Ala Glu Phe Gln Leu Asp Arg Arg Ala Val Met Ser Leu Asn	
500 505 510	
gag gcg gac gtg ggc tac aac tgc agc acc agc ggg ggc gcc gcc ggc	1584
Glu Ala Asp Val Gly Tyr Asn Cys Ser Thr Ser Gly Gly Ala Ala Gly	
515 520 525	
cgc ggc gcg ctg ggg ccc ttc ggc ctg ttc gtc ctc gcc gac cgc cgc	1632
Arg Gly Ala Leu Gly Pro Phe Gly Leu Phe Val Leu Ala Asp Arg Arg	
530 535 540	
ctc cgc cgc gag cag acg gcc gtc tac ttc tac gtg gcc aag ggc ctg	1680
Leu Arg Arg Glu Gln Thr Ala Val Tyr Phe Tyr Val Ala Lys Gly Leu	
545 550 555 560	
gac ggc tcc ctc gcc acg cac ttc tgc cag gac gag tcc cgc tcc tcc	1728
Asp Gly Ser Leu Ala Thr His Phe Cys Gln Asp Glu Ser Arg Ser Ser	
565 570 575	
agc gcc acc gac atc gtc aag cgc gtc gtc ggc agc gcc gtc ccc gtg	1776
Ser Ala Thr Asp Ile Val Lys Arg Val Val Gly Ser Ala Val Pro Val	
580 585 590	
ctg gag gac gag gcc acg ctc tcg ctc cgg gtg ctc gtc gac cac tcc	1824
Leu Glu Asp Glu Ala Thr Leu Ser Leu Arg Val Leu Val Asp His Ser	
595 600 605	
atc gtc gag agc ttc gcg cag ggc ggg agg tcc acc gcc aca tcg cgc	1872
Ile Val Glu Ser Phe Ala Gln Gly Gly Arg Ser Thr Ala Thr Ser Arg	
610 615 620	
gtc tac ccc acc gag gcc atc tac gcc aac gcc ggc gtc ttc ctc ttc	1920
Val Tyr Pro Thr Glu Ala Ile Tyr Ala Asn Ala Gly Val Phe Leu Phe	
625 630 635 640	
aac aac gcc acc gcc gcg cgg gtc acg gcc acg aag ctc gtc gtc cac	1968
Asn Asn Ala Thr Ala Ala Arg Val Thr Ala Thr Lys Leu Val Val His	
645 650 655	
gag atg gac tcg tca tac aac cac gac tac atg gcg ccg gtg gca gac	2016
Glu Met Asp Ser Ser Tyr Asn His Asp Tyr Met Ala Pro Val Ala Asp	
660 665 670	
atc tga	2022
Ile *	

<210> SEQ ID NO 21
 <211> LENGTH: 673
 <212> TYPE: PRT
 <213> ORGANISM: Zea mays

<400> SEQUENCE: 21

Met Glu Thr Arg Asp Thr Asp Ala Thr Pro Leu Pro Tyr Ser Tyr Thr	
1 5 10 15	
Pro Leu Pro Ala Ala Asp Ala Ala Ser Ala Glu Val Ser Gly Thr Gly	
20 25 30	
Arg Thr Arg Ser Arg Arg Arg Pro Leu Cys Ala Ala Ala Leu Val Leu	
35 40 45	
Ser Ala Ala Leu Leu Leu Ala Val Ala Ala Leu Val Gly Val Gly Ser	
50 55 60	
Arg Pro Gly Ala Val Gly Met Thr Glu Ser Ala Ala Ser Ser Pro Thr	
65 70 75 80	
Pro Ser Arg Ser Arg Gly Pro Glu Ala Gly Val Ser Glu Lys Thr Ser	
85 90 95	
Gly Ala Ser Asp Asp Gly Gly Arg Leu Arg Gly Ala Gly Gly Asn Ala	
100 105 110	
Phe Pro Trp Ser Asn Ala Met Leu Gln Trp Gln Arg Thr Gly Phe His	
115 120 125	

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545		550		555		560
Asp Gly Ser Leu	Ala Thr His Phe Cys Gln Asp Glu Ser Arg Ser Ser					
	565			570		575
Ser Ala Thr Asp	Ile Val Lys Arg Val Val Gly Ser Ala Val Pro Val					
	580		585		590	
Leu Glu Asp Glu	Ala Thr Leu Ser Leu Arg Val Leu Val Asp His Ser					
	595		600		605	
Ile Val Glu Ser	Phe Ala Gln Gly Gly Arg Ser Thr Ala Thr Ser Arg					
	610		615		620	
Val Tyr Pro Thr	Glu Ala Ile Tyr Ala Asn Ala Gly Val Phe Leu Phe					
	625		630		635	640
Asn Asn Ala Thr	Ala Ala Arg Val Thr Ala Thr Lys Leu Val Val His					
	645		650		655	
Glu Met Asp Ser	Ser Tyr Asn His Asp Tyr Met Ala Pro Val Ala Asp					
	660		665		670	

Ile

<210> SEQ ID NO 22
 <211> LENGTH: 1638
 <212> TYPE: DNA
 <213> ORGANISM: Zea mays
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1) ... (1638)

<400> SEQUENCE: 22

atg ggc ctg ggt ttg gga gct ctt ctc aaa tcc ggc ggg ctc tcg gtc	48
Met Gly Leu Gly Leu Gly Ala Leu Leu Lys Ser Gly Gly Leu Ser Val	
1 5 10 15	
tcg gat cac gac gcc atc gtc tcg att aac atc ttc atc gcg ctg ctc	96
Ser Asp His Asp Ala Ile Val Ser Ile Asn Ile Phe Ile Ala Leu Leu	
20 25 30	
tgc agc tgc att gtc atc ggc cac ttg ctg gaa ggg aac cga tgg gtg	144
Cys Ser Cys Ile Val Ile Gly His Leu Leu Glu Gly Asn Arg Trp Val	
35 40 45	
aac gag tcc atc acc gcg ctt gtc atg ggc ctc atc acc gga ggc gtc	192
Asn Glu Ser Ile Thr Ala Leu Val Met Gly Leu Ile Thr Gly Gly Val	
50 55 60	
atc ctg ctg gtt act aat ggg aca aac tca cgc att ctt gtg ttc agc	240
Ile Leu Leu Val Thr Asn Gly Thr Asn Ser Arg Ile Leu Val Phe Ser	
65 70 75 80	
gag gac ctg ttt ttc ata tat tta ctt ccg ccg ata atc ttc aat gcc	288
Glu Asp Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala	
85 90 95	
ggg ttt caa gta aag aaa aag caa ttc ttc cgc aac ttt ata acg att	336
Gly Phe Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Ile Thr Ile	
100 105 110	
att ttg ttt ggt gct att ggg act ctg att tcc ttt gta ata atc tct	384
Ile Leu Phe Gly Ala Ile Gly Thr Leu Ile Ser Phe Val Ile Ile Ser	
115 120 125	
ctt ggt gct atg ggg ttg ttc aag aaa ctt gat gtt ggt cca ctc gag	432
Leu Gly Ala Met Gly Leu Phe Lys Lys Leu Asp Val Gly Pro Leu Glu	
130 135 140	
ctt ggg gac tat ctt gca att ggt gct att ttc tcg gca aca gat tct	480
Leu Gly Asp Tyr Leu Ala Ile Gly Ala Ile Phe Ser Ala Thr Asp Ser	
145 150 155 160	
gtt tgc acc tta cag gtg ctt aac cag gat gaa aca ccc cta ctc tat	528
Val Cys Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Leu Leu Tyr	
165 170 175	

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agt cta gtt ttt ggt gaa ggt gtt gtt aat gat gcc aca tct gtt gtg	576
Ser Leu Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Val Val	
180 185 190	
ctc ttc aat gca att gaa aac ctt gat att gat aat ttt gat gct att	624
Leu Phe Asn Ala Ile Glu Asn Leu Asp Ile Asp Asn Phe Asp Ala Ile	
195 200 205	
gtt ctg ttg aat ttc gtc gga aaa ttt ctc tac ttg ttc ttc acc agc	672
Val Leu Leu Asn Phe Val Gly Lys Phe Leu Tyr Leu Phe Phe Thr Ser	
210 215 220	
acc ata ctt gga gta gct acc ggg ttg ctt agt gca tac att atc aag	720
Thr Ile Leu Gly Val Ala Thr Gly Leu Leu Ser Ala Tyr Ile Ile Lys	
225 230 235 240	
aag ctc tgt ttt gcc aga cat tca act gat aga gaa gtt tct atc atg	768
Lys Leu Cys Phe Ala Arg His Ser Thr Asp Arg Glu Val Ser Ile Met	
245 250 255	
ata ctc atg gca tac ctt tca tac atg ata tca atg ctg ttg gac ctg	816
Ile Leu Met Ala Tyr Leu Ser Tyr Met Ile Ser Met Leu Leu Asp Leu	
260 265 270	
agt gga att ctt act gtc ttc ttc tgt gga ata gta atg tca cat tac	864
Ser Gly Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr	
275 280 285	
act tgg cat aat gtg aca gaa agt tct agg gtt acc acc aag cat act	912
Thr Trp His Asn Val Thr Glu Ser Ser Arg Val Thr Thr Lys His Thr	
290 295 300	
ttt gca act tta tca ttc att gca gaa att ttc ctc ttc ctc tat gtt	960
Phe Ala Thr Leu Ser Phe Ile Ala Glu Ile Phe Leu Phe Leu Tyr Val	
305 310 315 320	
ggg atg gat gca ttg gac att gag aag tgg aaa tta gct agt agc agt	1008
Gly Met Asp Ala Leu Asp Ile Glu Lys Trp Lys Leu Ala Ser Ser Ser	
325 330 335	
cct aag aaa cca att gct tta agt gca att att ttg ggc ttg gtt atg	1056
Pro Lys Lys Pro Ile Ala Leu Ser Ala Ile Ile Leu Gly Leu Val Met	
340 345 350	
gtt gga aga gcg gca ttt gta ttc cct ttg tcg ttc tta tcc aac cta	1104
Val Gly Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu	
355 360 365	
agc aaa aag gag gcc cgt cca aag atc tcc ttc aag caa caa gta atc	1152
Ser Lys Lys Glu Ala Arg Pro Lys Ile Ser Phe Lys Gln Gln Val Ile	
370 375 380	
ata tgg tgg gct ggt ctc atg aga gga gca gtg tca att gcg ctt gcc	1200
Ile Trp Trp Ala Gly Leu Met Arg Gly Ala Val Ser Ile Ala Leu Ala	
385 390 395 400	
tat aac aag ttt aca gca tct ggt cac act gaa gtg cga gtc aat gct	1248
Tyr Asn Lys Phe Thr Ala Ser Gly His Thr Glu Val Arg Val Asn Ala	
405 410 415	
atc atg atc acc agc aca gtt att gtt gtt cta ttc agc aca atg gtt	1296
Ile Met Ile Thr Ser Thr Val Ile Val Val Leu Phe Ser Thr Met Val	
420 425 430	
ttc ggc ctg ctg acg aag ccg ctg ctc agt ctc ctc atc cca cca agg	1344
Phe Gly Leu Leu Thr Lys Pro Leu Leu Ser Leu Leu Ile Pro Pro Arg	
435 440 445	
act gga ctg aac acg tcg tct ctg ctc tca agc cag tct atg ctg gac	1392
Thr Gly Leu Asn Thr Ser Leu Leu Ser Ser Gln Ser Met Leu Asp	
450 455 460	
cca ctc ctt act agc atg atg ggg tct gac ttt gat gta ggg cag atc	1440
Pro Leu Leu Thr Ser Met Met Gly Ser Asp Phe Asp Val Gly Gln Ile	
465 470 475 480	
aac tcc cct caa tac aac ctc cag ttc att ctc acc gcg cca gct cgc	1488
Asn Ser Pro Gln Tyr Asn Leu Gln Phe Ile Leu Thr Ala Pro Ala Arg	

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485	490	495	
tcc gtc cat cgc ctt tgg cgc aag ttt gac gat cgg ttc atg cgc ccg			1536
Ser Val His Arg Leu Trp Arg Lys Phe Asp Asp Arg Phe Met Arg Pro			
500	505	510	
gtg ttc ggg ggg cga ggt ttc gtc ccc ttt gtg cct ggt tcg ccg gtg			1584
Val Phe Gly Gly Arg Gly Phe Val Pro Phe Val Pro Gly Ser Pro Val			
515	520	525	
gag agg agt gtc cct gaa tct cac ctg ggc act gtg acg gag gct gag			1632
Glu Arg Ser Val Pro Glu Ser His Leu Gly Thr Val Thr Glu Ala Glu			
530	535	540	
ggc agt			1638
Gly Ser			
545			
<210> SEQ ID NO 23			
<211> LENGTH: 546			
<212> TYPE: PRT			
<213> ORGANISM: Zea mays			
<400> SEQUENCE: 23			
Met Gly Leu Gly Leu Gly Ala Leu Leu Lys Ser Gly Gly Leu Ser Val			
1	5	10	15
Ser Asp His Asp Ala Ile Val Ser Ile Asn Ile Phe Ile Ala Leu Leu			
20	25	30	
Cys Ser Cys Ile Val Ile Gly His Leu Leu Glu Gly Asn Arg Trp Val			
35	40	45	
Asn Glu Ser Ile Thr Ala Leu Val Met Gly Leu Ile Thr Gly Gly Val			
50	55	60	
Ile Leu Leu Val Thr Asn Gly Thr Asn Ser Arg Ile Leu Val Phe Ser			
65	70	75	80
Glu Asp Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala			
85	90	95	
Gly Phe Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Ile Thr Ile			
100	105	110	
Ile Leu Phe Gly Ala Ile Gly Thr Leu Ile Ser Phe Val Ile Ile Ser			
115	120	125	
Leu Gly Ala Met Gly Leu Phe Lys Lys Leu Asp Val Gly Pro Leu Glu			
130	135	140	
Leu Gly Asp Tyr Leu Ala Ile Gly Ala Ile Phe Ser Ala Thr Asp Ser			
145	150	155	160
Val Cys Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Leu Leu Tyr			
165	170	175	
Ser Leu Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Val Val			
180	185	190	
Leu Phe Asn Ala Ile Glu Asn Leu Asp Ile Asp Asn Phe Asp Ala Ile			
195	200	205	
Val Leu Leu Asn Phe Val Gly Lys Phe Leu Tyr Leu Phe Phe Thr Ser			
210	215	220	
Thr Ile Leu Gly Val Ala Thr Gly Leu Leu Ser Ala Tyr Ile Ile Lys			
225	230	235	240
Lys Leu Cys Phe Ala Arg His Ser Thr Asp Arg Glu Val Ser Ile Met			
245	250	255	
Ile Leu Met Ala Tyr Leu Ser Tyr Met Ile Ser Met Leu Leu Asp Leu			
260	265	270	
Ser Gly Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr			
275	280	285	

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Thr Trp His Asn Val Thr Glu Ser Ser Arg Val Thr Thr Lys His Thr
 290 295 300

Phe Ala Thr Leu Ser Phe Ile Ala Glu Ile Phe Leu Phe Leu Tyr Val
 305 310 315 320

Gly Met Asp Ala Leu Asp Ile Glu Lys Trp Lys Leu Ala Ser Ser Ser
 325 330 335

Pro Lys Lys Pro Ile Ala Leu Ser Ala Ile Ile Leu Gly Leu Val Met
 340 345 350

Val Gly Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu
 355 360 365

Ser Lys Lys Glu Ala Arg Pro Lys Ile Ser Phe Lys Gln Gln Val Ile
 370 375 380

Ile Trp Trp Ala Gly Leu Met Arg Gly Ala Val Ser Ile Ala Leu Ala
 385 390 395 400

Tyr Asn Lys Phe Thr Ala Ser Gly His Thr Glu Val Arg Val Asn Ala
 405 410 415

Ile Met Ile Thr Ser Thr Val Ile Val Val Leu Phe Ser Thr Met Val
 420 425 430

Phe Gly Leu Leu Thr Lys Pro Leu Leu Ser Leu Leu Ile Pro Pro Arg
 435 440 445

Thr Gly Leu Asn Thr Ser Ser Leu Leu Ser Ser Gln Ser Met Leu Asp
 450 455 460

Pro Leu Leu Thr Ser Met Met Gly Ser Asp Phe Asp Val Gly Gln Ile
 465 470 475 480

Asn Ser Pro Gln Tyr Asn Leu Gln Phe Ile Leu Thr Ala Pro Ala Arg
 485 490 495

Ser Val His Arg Leu Trp Arg Lys Phe Asp Asp Arg Phe Met Arg Pro
 500 505 510

Val Phe Gly Gly Arg Gly Phe Val Pro Phe Val Pro Gly Ser Pro Val
 515 520 525

Glu Arg Ser Val Pro Glu Ser His Leu Gly Thr Val Thr Glu Ala Glu
 530 535 540

Gly Ser
 545

<210> SEQ ID NO 24
 <211> LENGTH: 2286
 <212> TYPE: DNA
 <213> ORGANISM: Zea mays
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)...(2286)

<400> SEQUENCE: 24

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1 5 10 15	
gcc gtc atc ggc atc gcc ttc gcc gtc gtg cag tgg gtg gtc gtg tcg	96
Ala Val Ile Gly Ile Ala Phe Ala Val Val Gln Trp Val Val Val Ser	
20 25 30	
cgc gtg aag ctc tcc ccg gcc gcg tcc gcc gcc agc gcc gcc aag gcc	144
Arg Val Lys Leu Ser Pro Ala Ala Ser Gly Gly Ser Gly Gly Lys Ala	
35 40 45	
ggc tac gcc gac tcc ctc atc gag gag gag gag ggg ctc aac gac cac	192
Gly Tyr Ala Asp Ser Leu Ile Glu Glu Glu Glu Gly Leu Asn Asp His	
50 55 60	

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aac gtc gtc gtc aag tgc gcc gag atc cag aac gcc atc tcc gaa gga	240
Asn Val Val Val Lys Cys Ala Glu Ile Gln Asn Ala Ile Ser Glu Gly	
65 70 75 80	
gca aca tcg ttt ctt ttc acc gag tac caa tat gtt ggt atc ttc atg	288
Ala Thr Ser Phe Leu Phe Thr Glu Tyr Gln Tyr Val Gly Ile Phe Met	
85 90 95	
gct atc ttc gct gtt gtg atc ttc ctc ttc ctt ggt tcg gtt gag gga	336
Ala Ile Phe Ala Val Val Ile Phe Leu Phe Leu Gly Ser Val Glu Gly	
100 105 110	
ttc agc acg aag agc cag ccc tgc aca tat agc aag gac aag tac tgc	384
Phe Ser Thr Lys Ser Gln Pro Cys Thr Tyr Ser Lys Asp Lys Tyr Cys	
115 120 125	
aag cct gcg ctg ttc act gca ctc ttt agc act gtg tcc ttc ttg ctt	432
Lys Pro Ala Leu Phe Thr Ala Leu Phe Ser Thr Val Ser Phe Leu Leu	
130 135 140	
gga gcc atc acc tct ctg gtc tct ggt ttc ctt ggc atg aag att gcc	480
Gly Ala Ile Thr Ser Leu Val Ser Gly Phe Leu Gly Met Lys Ile Ala	
145 150 155 160	
aca tat gcg aat gcc aga act acc ctg gaa gct agg aag ggt gtt ggc	528
Thr Tyr Ala Asn Ala Arg Thr Thr Leu Glu Ala Arg Lys Gly Val Gly	
165 170 175	
aag gct ttt atc act gct ttc cgc tct ggc gct gtt atg ggt ttc ctg	576
Lys Ala Phe Ile Thr Ala Phe Arg Ser Gly Ala Val Met Gly Phe Leu	
180 185 190	
ctt gca tca agt ggg ctt gtg gtt ctg tac atc aca att aat gta ttt	624
Leu Ala Ser Ser Gly Leu Val Val Leu Tyr Ile Thr Ile Asn Val Phe	
195 200 205	
aag ttg tat tac ggt gat gac tgg gag ggt ctt ttt gag tcc atc act	672
Lys Leu Tyr Tyr Gly Asp Asp Trp Glu Gly Leu Phe Glu Ser Ile Thr	
210 215 220	
ggc tat ggt ctt ggt ggg tcg tcc atg gct ctc ttc gga aga gtt ggt	720
Gly Tyr Gly Leu Gly Gly Ser Ser Met Ala Leu Phe Gly Arg Val Gly	
225 230 235 240	
gga ggt atc tac aca aag gct gct gat gtt ggt gcc gat ctt gtt gga	768
Gly Gly Ile Tyr Thr Lys Ala Ala Asp Val Gly Ala Asp Leu Val Gly	
245 250 255	
aag gtc gag agg aac att cct gag gat gat cct agg aac cca gct gtg	816
Lys Val Glu Arg Asn Ile Pro Glu Asp Asp Pro Arg Asn Pro Ala Val	
260 265 270	
att gct gat aat gtc ggt gac aat gtt ggt gac att gct gga atg gga	864
Ile Ala Asp Asn Val Gly Asp Asn Val Gly Asp Ile Ala Gly Met Gly	
275 280 285	
tct gat ctc ttt ggg tca tac gca gag tct tct tgt gct gcc ctt gtt	912
Ser Asp Leu Phe Gly Ser Tyr Ala Glu Ser Ser Cys Ala Ala Leu Val	
290 295 300	
gtt gcg tct att tca tct ttc gga atc gac cat gat ttc act ggg atg	960
Val Ala Ser Ile Ser Ser Phe Gly Ile Asp His Asp Phe Thr Gly Met	
305 310 315 320	
tgc tac cca ctc ctt gtt agc tct gtt ggt atc att gtc tgc ttg atc	1008
Cys Tyr Pro Leu Leu Val Ser Ser Val Gly Ile Ile Val Cys Leu Ile	
325 330 335	
acc acc ctt ttt gct act gat ttc ttt gaa gtc aag gct gtg aaa gaa	1056
Thr Thr Leu Phe Ala Thr Asp Phe Phe Glu Val Lys Ala Val Lys Glu	
340 345 350	
att gag cct gca ctt aag aag cag ctc atc atc tcc acc gtc ctg atg	1104
Ile Glu Pro Ala Leu Lys Lys Gln Leu Ile Ile Ser Thr Val Leu Met	
355 360 365	
act ttt ggt att gct cta atc agc tgg ttg gcc ctt cca gct aag ttc	1152
Thr Phe Gly Ile Ala Leu Ile Ser Trp Leu Ala Leu Pro Ala Lys Phe	
370 375 380	

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acc atc tac aac ttc ggt act cag aag gag gtt tcc aac tgg ggt ttg	1200
Thr Ile Tyr Asn Phe Gly Thr Gln Lys Glu Val Ser Asn Trp Gly Leu	
385 390 395 400	
ttc ttc tgt gtt tca att ggt ctg tgg gct ggt ttg att att ggt ttt	1248
Phe Phe Cys Val Ser Ile Gly Leu Trp Ala Gly Leu Ile Ile Gly Phe	
405 410 415	
gtc aca gaa tac tac act agc aat gca tac agt cct gtg caa gat gtt	1296
Val Thr Glu Tyr Tyr Thr Ser Asn Ala Tyr Ser Pro Val Gln Asp Val	
420 425 430	
gcg gat tcg tgc aga act ggt gct gcc act aat gtc att ttt ggt ctt	1344
Ala Asp Ser Cys Arg Thr Gly Ala Ala Thr Asn Val Ile Phe Gly Leu	
435 440 445	
gct ctt gga tac aag tct gtt atc atc ccg att ttc gct att gct gtt	1392
Ala Leu Gly Tyr Lys Ser Val Ile Ile Pro Ile Phe Ala Ile Ala Val	
450 455 460	
agc atc tat gtc agt ttc tcc att gct gcg atg tac ggc att gca gtt	1440
Ser Ile Tyr Val Ser Phe Ser Ile Ala Ala Met Tyr Gly Ile Ala Val	
465 470 475 480	
gcc gct ctt ggt atg ctg agc aca atc gca act ggt ctt gct att gat	1488
Ala Ala Leu Gly Met Leu Ser Thr Ile Ala Thr Gly Leu Ala Ile Asp	
485 490 495	
gct tat ggt ccc atc agt gac aat gct ggt ggt att gct gag atg gct	1536
Ala Tyr Gly Pro Ile Ser Asp Asn Ala Gly Gly Ile Ala Glu Met Ala	
500 505 510	
gga atg agc cac aga atc cgt gag aga act gat gct ctt gat gct gct	1584
Gly Met Ser His Arg Ile Arg Glu Arg Thr Asp Ala Leu Asp Ala Ala	
515 520 525	
ggc aac aca act gct gct att gga aag ggg ttt gcc att ggt tca gct	1632
Gly Asn Thr Thr Ala Ala Ile Gly Lys Gly Phe Ala Ile Gly Ser Ala	
530 535 540	
gct ctt gtg tcc ctg gcg ctt ttt ggt gcc ttt gtc agc aga gct gga	1680
Ala Leu Val Ser Leu Ala Leu Phe Gly Ala Phe Val Ser Arg Ala Gly	
545 550 555 560	
gtg aag gtc gtc gac gtc ctc tcc ccc aag gtt ttc att ggt ttg att	1728
Val Lys Val Val Asp Val Leu Ser Pro Lys Val Phe Ile Gly Leu Ile	
565 570 575	
gtt gga gcc atg ctt ccg tac tgg ttc tct gcc atg acc atg aag agt	1776
Val Gly Ala Met Leu Pro Tyr Trp Phe Ser Ala Met Thr Met Lys Ser	
580 585 590	
gtt gga agc gct gcc ctg aag atg gtg gag gag gtc cgc agg cag ttc	1824
Val Gly Ser Ala Ala Leu Lys Met Val Glu Glu Val Arg Arg Gln Phe	
595 600 605	
aac acc att cct ggg ttg atg gag gga aca gcc aag ccc gac tac gca	1872
Asn Thr Ile Pro Gly Leu Met Glu Gly Thr Ala Lys Pro Asp Tyr Ala	
610 615 620	
acc tgt gtg aag atc tcc act gat gct tcc atc aag gag atg att cct	1920
Thr Cys Val Lys Ile Ser Thr Asp Ala Ser Ile Lys Glu Met Ile Pro	
625 630 635 640	
ccg ggc gct ctg gtc atg ctg act ccc ctc atc gtt gga acc ctc ttt	1968
Pro Gly Ala Leu Val Met Leu Thr Pro Leu Ile Val Gly Thr Leu Phe	
645 650 655	
ggc gtc gag act ctc tcc ggc gtt ctt gct ggt gcc ctg gtt tct gga	2016
Gly Val Glu Thr Leu Ser Gly Val Leu Ala Gly Ala Leu Val Ser Gly	
660 665 670	
gtg cag atc gcc atc tct gct tcc aac acc ggc ggt gca tgg gac aat	2064
Val Gln Ile Ala Ile Ser Ala Ser Asn Thr Gly Gly Ala Trp Asp Asn	
675 680 685	
gcc aag aag tac atc gag gct ggt gcc agc gag cac gcg agg acc ctc	2112
Ala Lys Lys Tyr Ile Glu Ala Gly Ala Ser Glu His Ala Arg Thr Leu	

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690	695	700	
ggt ccc aag gga tcc gac tgc cac aag gcc gct gtg atc ggt gac acc			2160
Gly Pro Lys Gly Ser Asp Cys His Lys Ala Ala Val Ile Gly Asp Thr			
705	710	715	720
att ggt gac ccc ctg aag gac acc tcc ggc ccg tcc ctc aac atc ctc			2208
Ile Gly Asp Pro Leu Lys Asp Thr Ser Gly Pro Ser Leu Asn Ile Leu			
	725	730	735
atc aag ctc atg gcc gtg gag tcc ctc gtg ttt gcc ccc ttc ttt gcc			2256
Ile Lys Leu Met Ala Val Glu Ser Leu Val Phe Ala Pro Phe Phe Ala			
	740	745	750
acc cag ggt ggc ctg ctc ttc aag tac ctg			2286
Thr Gln Gly Gly Leu Leu Phe Lys Tyr Leu			
	755	760	
<p><210> SEQ ID NO 25 <211> LENGTH: 762 <212> TYPE: PRT <213> ORGANISM: Zea mays</p>			
<p><400> SEQUENCE: 25</p>			
Met Ala Ile Leu Ser Ala Leu Ala Thr Glu Val Leu Ile Pro Val Ala			
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Ala Val Ile Gly Ile Ala Phe Ala Val Val Gln Trp Val Val Val Ser			
	20	25	30
Arg Val Lys Leu Ser Pro Ala Ala Ser Gly Gly Ser Gly Gly Lys Ala			
	35	40	45
Gly Tyr Ala Asp Ser Leu Ile Glu Glu Glu Gly Leu Asn Asp His			
	50	55	60
Asn Val Val Val Lys Cys Ala Glu Ile Gln Asn Ala Ile Ser Glu Gly			
	65	70	75
Ala Thr Ser Phe Leu Phe Thr Glu Tyr Gln Tyr Val Gly Ile Phe Met			
	85	90	95
Ala Ile Phe Ala Val Val Ile Phe Leu Phe Leu Gly Ser Val Glu Gly			
	100	105	110
Phe Ser Thr Lys Ser Gln Pro Cys Thr Tyr Ser Lys Asp Lys Tyr Cys			
	115	120	125
Lys Pro Ala Leu Phe Thr Ala Leu Phe Ser Thr Val Ser Phe Leu Leu			
	130	135	140
Gly Ala Ile Thr Ser Leu Val Ser Gly Phe Leu Gly Met Lys Ile Ala			
	145	150	155
Thr Tyr Ala Asn Ala Arg Thr Thr Leu Glu Ala Arg Lys Gly Val Gly			
	165	170	175
Lys Ala Phe Ile Thr Ala Phe Arg Ser Gly Ala Val Met Gly Phe Leu			
	180	185	190
Leu Ala Ser Ser Gly Leu Val Val Leu Tyr Ile Thr Ile Asn Val Phe			
	195	200	205
Lys Leu Tyr Tyr Gly Asp Asp Trp Glu Gly Leu Phe Glu Ser Ile Thr			
	210	215	220
Gly Tyr Gly Leu Gly Gly Ser Ser Met Ala Leu Phe Gly Arg Val Gly			
	225	230	235
Gly Gly Ile Tyr Thr Lys Ala Ala Asp Val Gly Ala Asp Leu Val Gly			
	245	250	255
Lys Val Glu Arg Asn Ile Pro Glu Asp Asp Pro Arg Asn Pro Ala Val			
	260	265	270
Ile Ala Asp Asn Val Gly Asp Asn Val Gly Asp Ile Ala Gly Met Gly			
	275	280	285

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Ser Asp Leu Phe Gly Ser Tyr Ala Glu Ser Ser Cys Ala Ala Leu Val
 290 295 300

Val Ala Ser Ile Ser Ser Phe Gly Ile Asp His Asp Phe Thr Gly Met
 305 310 315 320

Cys Tyr Pro Leu Leu Val Ser Ser Val Gly Ile Ile Val Cys Leu Ile
 325 330 335

Thr Thr Leu Phe Ala Thr Asp Phe Phe Glu Val Lys Ala Val Lys Glu
 340 345 350

Ile Glu Pro Ala Leu Lys Lys Gln Leu Ile Ile Ser Thr Val Leu Met
 355 360 365

Thr Phe Gly Ile Ala Leu Ile Ser Trp Leu Ala Leu Pro Ala Lys Phe
 370 375 380

Thr Ile Tyr Asn Phe Gly Thr Gln Lys Glu Val Ser Asn Trp Gly Leu
 385 390 395 400

Phe Phe Cys Val Ser Ile Gly Leu Trp Ala Gly Leu Ile Ile Gly Phe
 405 410 415

Val Thr Glu Tyr Tyr Thr Ser Asn Ala Tyr Ser Pro Val Gln Asp Val
 420 425 430

Ala Asp Ser Cys Arg Thr Gly Ala Ala Thr Asn Val Ile Phe Gly Leu
 435 440 445

Ala Leu Gly Tyr Lys Ser Val Ile Ile Pro Ile Phe Ala Ile Ala Val
 450 455 460

Ser Ile Tyr Val Ser Phe Ser Ile Ala Ala Met Tyr Gly Ile Ala Val
 465 470 475 480

Ala Ala Leu Gly Met Leu Ser Thr Ile Ala Thr Gly Leu Ala Ile Asp
 485 490 495

Ala Tyr Gly Pro Ile Ser Asp Asn Ala Gly Gly Ile Ala Glu Met Ala
 500 505 510

Gly Met Ser His Arg Ile Arg Glu Arg Thr Asp Ala Leu Asp Ala Ala
 515 520 525

Gly Asn Thr Thr Ala Ala Ile Gly Lys Gly Phe Ala Ile Gly Ser Ala
 530 535 540

Ala Leu Val Ser Leu Ala Leu Phe Gly Ala Phe Val Ser Arg Ala Gly
 545 550 555 560

Val Lys Val Val Asp Val Leu Ser Pro Lys Val Phe Ile Gly Leu Ile
 565 570 575

Val Gly Ala Met Leu Pro Tyr Trp Phe Ser Ala Met Thr Met Lys Ser
 580 585 590

Val Gly Ser Ala Ala Leu Lys Met Val Glu Glu Val Arg Arg Gln Phe
 595 600 605

Asn Thr Ile Pro Gly Leu Met Glu Gly Thr Ala Lys Pro Asp Tyr Ala
 610 615 620

Thr Cys Val Lys Ile Ser Thr Asp Ala Ser Ile Lys Glu Met Ile Pro
 625 630 635 640

Pro Gly Ala Leu Val Met Leu Thr Pro Leu Ile Val Gly Thr Leu Phe
 645 650 655

Gly Val Glu Thr Leu Ser Gly Val Leu Ala Gly Ala Leu Val Ser Gly
 660 665 670

Val Gln Ile Ala Ile Ser Ala Ser Asn Thr Gly Gly Ala Trp Asp Asn
 675 680 685

Ala Lys Lys Tyr Ile Glu Ala Gly Ala Ser Glu His Ala Arg Thr Leu
 690 695 700

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caaggcgcgga gacggcgggcg tcacacatcg ggcagttgg ttgggtcgag ctcccaacca 1740
actcgctccc ggcagcca agccagccac gacc 1774

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What is claimed is:

1. A method for increasing the rate or degree of silk exsertion in a transformed *Zea mays* plant, relative to a non-transformed *Zea mays* plant, comprising transforming said plant with a construct comprising a silk-specific or silk-preferred promoter comprising SEQ ID NO: 1 or SEQ ID NO: 26 operably linked to a polynucleotide encoding a sodium antiporter, vacuolar pyrophosphatase, soluble invertase, expansin, sucrose symporter or aquaporin, wherein expression of said linked polynucleotide increases the rate or degree of silk exsertion.

2. The method of claim 1 wherein said polynucleotide encodes an expansin protein.

3. The method of claim 2 wherein the polynucleotide encoding an expansin protein comprises SEQ ID NO: 8 or 10.

4. The method of claim 1 wherein said polynucleotide encodes an aquaporin.

5. The method of claim 4 wherein the polynucleotide encoding an aquaporin comprises SEQ ID NO: 12, 14, or 16.

6. The method of claim 1 wherein said polynucleotide encodes a sucrose symporter.

7. The method of claim 6 wherein said polynucleotide encoding a sucrose symporter comprises SEQ ID NO: 18.

8. The method of claim 1 wherein said polynucleotide encodes soluble invertase.

9. The method of claim 8 wherein the polynucleotide encoding soluble invertase comprises SEQ ID NO: 20.

10. The method of claim 1 wherein said polynucleotide encodes a sodium antiporter.

11. The method of claim 10 wherein the polynucleotide encoding a sodium antiporter comprises SEQ ID NO: 22.

12. The method of claim 1 wherein said polynucleotide encodes a vacuolar pyrophosphatase.

13. The method of claim 12, wherein the polynucleotide encoding a vacuolar pyrophosphatase comprises SEQ ID NO: 24.

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